1.

#### Title: Perfect score: Sequence: Database : Post-processing: Minimum Match 0% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 1000000 Scoring table: OM protein - protein search, using sw model Searched: Run on: al number of hits satisfying chosen parameters: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. A\_Geneseq\_36:\* PEP1 690 1 mdpqtapsrallllflhla.....rkmdrissssglgckvlrrh 134 188963 seqs, 23686106 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 April 27, 2000, 17:42:50 ; Search time 13.56 Seconds (without alignments) 234.066 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. SUMMARIES 188963

3333098 4333098	11110987654W21	Result
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121 ssssglgckvlrrh 134	61 qtsleplqesprptgywksrevategirghrkmvlytlraprspkmvggsgcfgrkmdri 120 	1 mdpqtapsrallllifihlafiggrshplgspgsasdletsglqeqrnhlqgklselqve 60 	Query Match 100.0%; Score 690; DB 1; Length 134; Best Local Similarity 100.0%; Pred. No. 8.1e-63; Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps	A. Takashima M;  30-269905/36.  brain natriuretic polypeptide - having smoot brain natriuretic polypeptide - having smoot brain natriuretic diuretic or natriuretic activ pressor activity.  4; Page 10; 16pp; English.  5; Page 10; 16pp; English.  4; Page 10; 16pp; English.  5; Page 10; 16pp; English.  6; Page 10; Page 10; Page 10; Page 10; Page 10;  6; Page 10; Pag	EP-385476-A. 05-SEP-1990. 01-MAR-1990; 104021. 01-MAR-1989; JP-049636. 10-MAR-1989; JP-059183. (DAPU) DAIICHI PURE KK. (DAPU) DAIICHI PHARM CO LTD. Sudoh T, Maekawa K, Minamino N, Kangawa K, Matsuo H;	Homo sapiens.  Location/Qualifiers  Rey  103. 134  protein  /label=mature hBNP  Disulphide_bonds112128  /note="feature of the mature protein"  peptide  /label="pre" sequence	ILT 1  RO6603 standard; protein; 134 AA.  RO6603; 11-JAN-1991 (first entry) Human Brain Natriuretic Polypeptide. Human brain natriuretic polypeptide (hBNP); clone hBNP-57;

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Matches 134
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31-MAY-1989; US-200383.
14-JUN-1988; US-2006470.
19-JAN-1989; US-299880.
(CALB) Calif Biotech Inc.
Seilhamer JJ, Lewicki J, So
                                                   18-MAR-1999.
10-SEP-1998; J04063.
11-SEP-1997; JP-246684.
(SHIO ) SHIONOGI & CO LTD.
Asada H, Endou K, Shimizu H
WPI; 99-243746/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New natriuretic and vasodilator peptides - obtd. using cDNA sequence encoding porcine brani natriuretic peptide and related human canine genes Example 5; Fig.5; 6lpp; English. Sequences derived from porcine brain natriuretic gene can be used in part as probes to isolate similar genes from different species. Although human natriuretic related peptides (NRP) could not be isolated directly, canine NRPs could be, and these could then be used as probes to their human equivalents. Here the gene product is shown, taken from the plasmid
                                                                                                                                                                                                                                                        25-JUN-1999 (first entry)
Human gamma-BNP protein sequence.
Gamma-BNP; human; brain natriuretic cardiac insufficiency; diagnosis.
     Sandwich
                             N-PSDB;
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Y05325;
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WPI; 90-007453/01.
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Protein encoded by human natriuretic related peptide.
Porcine BNP; natriuretic; diuretic; vasodilator; hypertension.
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Mismatches 0;
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MGPRWALPR-VLLLLFLHLLLLGCRSHPLGGAGLASEL--PGIQELLDRLRDRVSELQAE
qtsleplqesprptgvwksrevateg1rghrkmvlytlraprspkmvqgsgcfgrkmdr1

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R04084;
01-JUN-1990 (fir
011gopeptide enco
Porcine BNP; natr
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14-UUN-1988; US-2006470.
19-JAN-1989; US-29880.
(CALE) Calif Biotech Inc.
Seilhamer JJ, Lewicki J, S
                                                                                                                                                                                                                                                                                          mat_peptide
WO8912069-A.
14-DEC-1989.
31-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 20-21; 24pp; Japanese. This sequence is the human gamma-BNP (brain natriuretic protein). The invention relates to an immunoassay method specific for mammalia. gamma-BNP derivatives, which comprises the use of a first antibody reacting with mammalian alpha-BNP and a second antibody with preprogramma-BNP derivatives but not with alpha-BNP. The immunoassay is use for diagnosing and monitoring heart diseases, particularly cardiac insufficiency. The technique uses only blood plasma, and is simple, stable and reliable.
                                                                                         encoding porcine brani natriuretic peptide and related human canine genes Example 1; Fig. 1; 61pp; English.

Sequences derived from porcine brain natriuretic gene can be used in part as probes to isolate similar genes from different species. Although human natriuretic related peptides (NRP) could not be isolated directly, canine NRPs could be, and these could then be used as probes to their human
                                                                equivalents.
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encoded by porcine brain natriuretic peptide cDNA.
natriuretic; diuretic; vasodilator; hypertension.
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05-SEP-1990.
22-FEB-1989; 042720.
22-FEB-1989; JP-042720.
(DAUC) DALICHI PHARM CO
(DAIL-) DALICHI FHARM CO
(DAIL-) DALICHI AGAKU Y
WPI; 90-315501/42.
N-PSDB; 206197.
  14-DEC-1989;
31-MAY-1989;
31-MAY-1988;
14-JUN-1988;
                                                                                                    R04086 standard; protein; 131 AA.
R04086;
01-JUN-1990 (first entry)
Protein encoded by canine natriuretic related peptide.
Porcine BNP; natriuretic; diuretic; vasodilator; hyper
                                                                                        Key
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                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 5; 8pp; Japanese. CDNA encoding porcine BNP was isolated from mRNA obtained from atrial fibrillation. The nucleotide at position 170 is a pyram: The ambiguity leads to two possible protein sequences, one containing His at the corresponding site and the other containing. Tyr. The CDS is claimed.
                                       W08912069-A.
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Porcine Brain Natriuretic
Porcine Brain Natriuretic
Sus scrofa domestica.
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US-2006470.
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Pred. No. 6e-26;
0; Mismatches
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Matches 50
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Best Local Similarity
Matches 69; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JAN-1989; US-299880. (CALB) Callf Blotech Inc. Seilhamer JJ, Lewicki J, S WPI; 90-007453/01. N-PSDB; 002852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R62682;
14-JUL-1995 (1
Hamster brain r
                                                                                                                                                                                                                                                         N-PSDB; Q73026.

Hamster brain derived natriuretic peptide(s) - useful for detection of BNPs, and in vaccine production Claim 1; Page 5; 8pp; Japanese.
Q73026 encodes R62682 hamster brain natriuretic peptide R62682 can be used for the detection and determination owhich is useful for various reagents and medicines.

Sequence 122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New natriuretic and vasodilator peptides encoding porcine brani natriuretic peptide Example 4; Fig.3; 61pp; English.
Although human natriuretic related peptides directly, canine NRPs could be, and these c their human equivalents.

See also 003845.
                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1993; JP-067113.
(SHIO) SHIONOGI & CO LTD
WPI; 94-354771/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cricetulus griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-1995 (first entry)
Hamster brain natriuretic
Brain natriuretic peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-1994.
25-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J06279496-A.
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42
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                                                                                                                                                             1 Similarity
50; Conserv
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                                                                                                                                                             Conservative
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35.5%;
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23; Mismatches
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No. 2.7
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.9e-13;
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human canine
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Best Local S
Matches 42
Isolating DNA encoding rat brain natriuretic peptide(s) treating oedema hypertension congestive heart and renal claim 1; Page 1; 7pp; Japanese.
The N-terminal Met residue is optional. Expression vector containing DNA encoding this amino acid sequence are use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A new method for the isolation of peptide(s) - comprises fusing peptide to a granule forming protein and cleaving the peptide fr the resulting fusion protein using a protease Example 2; Page 12; 17pp; Japanese.

R72812 is a gamma-IFN/glucagon/BNP fusion protein, it was used to demonstrate a new method for the isolation of peptides. The fusion protein is recombinantly produced in transformed E. coli, the glucagon/BNP is then cleaved from the granule forming protein gamma-IFN, using a protease. The glucagon can now be isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gamma-IFN/glucagon/BNP fusion protein.
Gamma-IFN/glucagon/BNP; fusion protein; peptide isolation method;
granule forming protein; protease cleavage; E. coli;
B-type natriuretic peptide; gamma-interferon;
recombinant production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from the Sequence
                                                                  (MATS/) MATSUO H.
WPI; 91-076871/11.
N-PSDB; Q10572.
                                                                                                                                                                                                                                   Rattus.
                                                                                                                                                                                                                                                                  BNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1993; 236732.
22-SEP-1993; JP-236732.
(SHIO ) SHIONOGI & CO LTD.
WPI; 95-167255/22.
                                                                                                                                                                                                                                                                               Rat Brain Natriuretic
                                                                                                                                                                                                                                                                                                                        R10973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma-IFN, using a protease. from the cell culture.
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                                                                                                             31-JAN-1991.
19-JUN-1989; 157066.
19-JUN-1989; JP-157066
                                                                                                                                                      J03022986-A.
                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                         3-MAY-1991 (first entry)
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                                                                                                                                                                                                                                                                Brain Natriuretic peptide.
vasodepressor; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                     gsgcfgrkmdrissssglgckvlrrh 134
                                                                                                                                                                                                                                                                                                                                                                                           GSGCFGRKMDRISSSSGLGCKVLRRH 175
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                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                                                                                  /label- signal peptide
27. .121
/label- mature BNP
                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                      Protein;
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                                                                                                                                                                                                                                                                                                                       121
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Pred. No. 1.3e
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                                                                                                                                                                                                                                                                congestive heart failure;
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  Expression vectors sequence are used
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                                             failure
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RESULT R36381

R36381

standard;

Protein;

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29-JUL-1993 R36381;

(first entry)

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SPKMVQGSGCFGRKMDRISSSSGLGCKVLRRH

32

PRESENCE DE LA COMPTE DEL COMPTE DE LA COMPTE DEL LA COMPTE DE LA COMP

23-MAR-1993. 10-SEP-1991;

230597

J05068581-A. misc\_difference Synthetic.

/note=

"May be absent"

Location/Qualifiers

Recombinant hBNP.
Plasmid; fusion peptide;
brain natriuretic peptidi

peptide;

murine; le; hBNP;

recombinant; rat; interleukin

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IL-1;

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Best L
                                   Query Match
Best Local Similarity
Matches 32; Conserv
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                                                                                                        Asp in the be deleted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transform host cells. The brain natriuretic peptide Sequence 121 AA;
                                                                                                                                                     Physiologically active peptide prepn. e.g. human brain natriuretic peptide - by culturing transformed cells he which encodes fused protein of active and protective p collecting and cleaving protein
Disclosure; Page 6; 16pp; Japanese.
                                                                                                                                                                                                                  03-SEP-1991; 222783.
03-SEP-1991; JP-22783.
(DAIL) DAIICHI KAGAKU YAKUHIN (DAUC) DAIICHI PHARM CO LTD.
WPI; 93-120386/15
                                                                                                                                                                                                                                                                                         Homo sapiens. J05056794-A.
                                                                                                                                                                                                                                                                                                                                      R34301;
28-JUL-1993
                                                                                                                   Disclosure; Page 6; 16pp; Japanese.
The sequences given in R34301-02 are mutated brain nat
peptides (BNP). These peptides have been modified su
Asp in the N-terminal Asp-Pro linkage may be replaced
                                                                                                                                                                                                                                                                                                                Wild type;
                                                                                               Sequence
                                                                                                                                                                                                                                                                             09-MAR-1993
                                                                                                                                                                                                                                                                                                                            Mutated hBNP
                                                                                                                                                                                                                                                                                                                                                                R34301 standard; Protein;
            103
                                                                                                                                                                                                                                                                                                                                                                                                                           105
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spkmvqgsgcfgrkmdr1ssssglgckvlrrh 134
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                                                                                                                                                                                                                                                                                                                brain natriuretic peptide; BNP; modify; Asp-Pro
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                               AA;
                                              24.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transformants are cultured for treating hypertension,
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                                                 Score 169;
Pred. No.
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                                     Mismatches
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No. 3.4e-10;
                                                             DB 1;
                                                 3e-11;
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RESULT RA 0861 ID RA 1 ID RA 1
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W70090
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28-OCT 1998 (first entry)
Brain natriuretic peptide (BNP) 1.
BNP; brain natriuretic peptide; cardiac disease; cardiac hypertrophy; chronic heart failure; ischaemic cardiac disease; arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collecting desired peptide
Disclosure; Page 8; lipp; Japanese.
The prepn. of BNP comprises: (a) obtaining a fused protein protein of formula X-Glu-BNP, where X is a leader sequence of 70-170 amino acids (R45761); (b) cleaving the fused protein with a restriction enzyme that can cleave between Glu and BNP.
                                                                                       W70090;
28-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brain natriuretic peptide prepn. - by contg. desired sequence, cleaving with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BNP.
BNP; brain natriuretic peptide;
cloning; pucl19; protease V8.
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This sequence represent a recombinant human brain natriuretic peptide (hBNP). This protein was encoded by the fragments of plasmids given in Q4110-04 which encode fusion peptides of murine or rat interleukin 1 (IL-1) fused to hBNP. Fusion genes of this kind can be used to express recombinant BNP which lacks the Asp-Pro N-terminal bond. The Asp residue may be replaced by Ser or may be absent.
                                                                                                                                          W70090 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (c) collecting BNP.
The BNP sequence is shown in (Q47829) and
is given in (Q47831).
Sequence 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-1991; 043641.
08-MAR-1991; JP-043641.
(SHIO ) SHIONOGI & CO LTD.
WPI; 93-297469/38.
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J05207891-A.
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(DAII-) DAIICHI KAGAKU YAKUHIN KK.
(DAUC) DAIICHI PHARM CO LTD.
(DAUC) DAIICHI PHARM CO LTD.
WPI; 93-130645/16
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32; Conserv
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ilarity 100.0%;
Conservative (
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Pred. No. 7.3e-11;
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This represents a brain natriuretic peptide (BNP) sequence. The invention provides a composition for treating cardiac diseases associated with cardiac hypertrophy. The composition comprises an active ingredient capable of binding to the peptide receptor of GC-A and promoting production of CGMP. The drug composition may be used clinically to treat cardiac diseases caused by cardiac hypertrophy, including chronic heart failure, ischaemic cardiac diseases and arrhythmia. The active substance can bind to the natriuretic peptide receptor of GC-A and promote production of CGMP, effectively preventing cardiac hypertrophy and leading to improvement of the pulmonary blood circulation. The substance does not affect haemodynamic properties, blood pressure, heart beat and
                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (first entry)
Brain natriuretic peptide (BNP).
atrial natriuretic peptide; brain natriuretic peptide; ANP; BNP;
lipophilic substituent; hypertension; conjestive heart failure; oedema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGMP; pulmonary blood circulation; haemodynamic property. Unidentified.
W09834636-Al.
13-AUG-1998.
05-FEB-1998; J00483.
05-FEB-1997; JP-022594.
(SUNR ) SUNTORY LTD.
(SUNR ) SUNTORY LTD.
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Disulfide\_bond

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RESULT 15
R35490
ID R35490
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DT 26-AUG
DT Tyr hB
KW Human;
LT-NOV
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12-NOV-1992; 119353.
14-NOV-1991; JP-326961.
(SHIO ) SHIONOGI SELYAKU KK.
Igano K, Inouye K, Kono M,
WPI; 93-160757/20.
                                                                                                                                                                     Monoclonal antibody recognising the C-terminus of hBNP - for determining hBNP levels in blood plasma by immunoassay; useful for diagnosing hypertension
Disclosure; Page 9; 13pp; English.
This sequence represents Tyr-hBNP (human brain natriuretic peptide).
This peptide was used in determining the specificity of a monoclonal antibody (MAb) which recognises the C-terminal of hBNP. The MAb is produced by hydridoma BC203 (FERM BP-3515). The Tyr residue had to be added to the N-terminal of the hBNP as no other Tyr appears within the molecule and this residue was used to carry a label to allow detection of the hBNP/MAb complex.

Sequence 33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
EP-542255-A.
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15-OCT-1998.
06-APR-1998; DK0142.
04-APR-1997; US-043400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; brain natriuretic peptide; specificity; monoclonal; antibody; MAb; hBNP; hydridoma; BC203; label; detection; hBNP/MAb complex.
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SPKMVQGSGCFGRKMDRISSSSGLGCKVLRRH 33
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100.0%; Pr
                                                                                            24.5%; Score 169; DB 1; 100.0%; Pred. No. 7.6e-11;
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

April 27, 2000, 18:26:25; Search time 14.62 Seconds (without alignments) 432.332 Million cell updates/sec

Title:
Perfect score:
Sequence:

PEP1 690 1 mdpqtapsralllllflhla.....rkmdrissssglgckvlrrh 134

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

142080 segs, 47169319 residues

Searched:

Total number of hits satisfying chosen parameters:

142080

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR\_62:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

45	44	43	42	41	40	39	3 8	37	36	35	34	33	32	31
72	74	74	74	74.5	74.5	74.5	74.5	74.5	77	78	80.5	81	81.5	81.5
10.4	10.7	10.7	10.7	10.8	10.8	10.8	10.8	10.8	11.2	11.3	11.7	11.7	11.8	11.8
22	786	27	22	1081	1074	1072	1072	1065	36	22	1319	30	1677	118
Ŋ	ш	N	N	N	N	N	N	N	N	N	Н	N	N	N
JT0581	A47547	A33431	A36399	T13231	T13229	T13232	T13228	T13230	S15821	A35418	C43735	S01657	T14267	B54119
natriuretic peptid	serine proteinease	atrial natriuretic	C-type natriuretic	dachshund protein	dachshund protein	dachshund protein	dachshund protein	dachshund isoform	ventricular natriu	brain natriuretic	bcsC protein - Ace	atrial natriuretic	Xin protein, stage	C-type natriuretic

## ALIGNMENTS

A;Molecule type: protein A;Residues: 103-134 < KAND. Biochem. Biophys. Res. Commun. 167, 693-700, 1990 A;Title: Isolation and identification of human brain natriuretic peptides in cardiac A;Reference number: A90161; MUID:90211249 A;Accession: A34661 A;Accession: A34661 A;Molecule type: protein A;Residues: 27-58 < HIN> A;Accession: B34661 A;Molecule type: protein A;Residues: 103-134 < HI2> C;Genetics: C;Genetics: C;Genetics: C;Genetics: A;Cross-references: GDB:127884; OMIM:600295 A;Cross-references: GDB:127884; OMIM:600295 A;Cross-references: GDB:127884; OMIM:600295 A;Introns: 44/3; 130/1 C;Superfamily: natriuretic peptide A precursor C;Reywords: brain; diuretic; hormone; natriuretic; osmoregulation F;27-134/Product: brain gamma natriuretic factor #Status experimental <amf> F;103-134/Product: brain gamma natriuretic factor #Status experimental <amf> F;112-128/Disulfide bonds: #status predicted F;27-134/Product: brain gamma natriuretic peptide #status experimental <amf> F;112-128/Disulfide bonds: #status predicted</amf></amf></amf>	A;Title: Cloning and sequence analysis of cDNA encoding a precursor for human brain A;Reference number: A30163; MUID:89193743 A;Recession: A30163 A;Rocession: A30163; MUID:90902577 A;Recession: A34143; MUID:90092577 A;Recession: A34143	retic peptide. retic peptide. retic peptide. retic peptide. retic peptide.	RESULT 1 AWHUB Inatriuretic peptide B precursor - human Inatriuretic peptide B precursor - human Instriuretic peptide B precursor - human Instriuretic peptide; brain natriuretic protein pr In; Alternate names: brain natriuretic peptide; brain gamma natriuretic factor In; Contains: brain alpha natriuretic peptide; brain gamma natriuretic factor In; Species: Homo sapiens (man) In; Date: 07-Sep-1990 #sequence_revision 02-Dec-1994 #text_change 18-Jun-1999
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bra

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brain natriuretic factor precursor - pig
N;Alternate names: brain natriuretic factor 32
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 16-Jul-1999
C;Accession: A31676; A31517; S06359
R;Mackawa, K.; Sudoh, T.; Furusawa, M.; Minamino, N.; Kangawa, K.; Ohkubo, H.; Nakanishi Biochem. Biophys. Res. Commun. 157, 410-416, 1988
A;Fitle: Cloning and sequence analysis of cDNA encoding a precursor for porcine brain na A;Feference number: A31676; MUID:89061744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M25547; GB:J04708; GB:M22477; GB:M22478; NID:g164392; PIDN:AAA31 R;Minamino, N.; Kangawa, K.; Matsuo, H. Biochem. Biophys. Res. Commun. 130-409, 1988
A;Title: Isolation and identification of a high molecular weight brain natriuretic pept A;Reference number: A31675; MUID:89061743
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 27-reb-1990 #seguence_revision 27-Feb-1990 #text_change 16-Jul-1999
C;Accession: A33873; A31675
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A; Residues: 26-131 <MIN>
C; Superfamily: natriuretic peptide A precursor
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A;Title: Cloning of a cDNA encoding porcine brain natriuretic peptide.
A;Reference number: A33873; MUID:89214071
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A; Accession: A31676
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A; Residues: 1-131 <POR>
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; Pred. No. 2.6e-25;
20; Mismatches 40;
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Pred. No. 2.1e-59;
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hplgspgsasdletsglgegrnhlggklselqvegtsleplgesprptgvwksrevateg HPVGGPGPVSEL--PGLQELLDRLRDRVSELQAEQLRVEPLQQGQGLEETWDSPAAAPAG

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A; Molecule type: protein
A; Residues: 100-131 <SUD>
R; Sudoh, T; Kangawa, K; Mi
Nature 332, 78-81, 1988
A; Title: A new natriuretic p
A; Reference number: S06359; J
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                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-103 <NGU>
R;Nguyen, T.T.; Lazure, C.; Babinski, K.;
Endocrinology 124, 1591-1593, 1989
Endocrinology 124, 1591-1593, 1989
A;Title: Aldosterone secretion inhibitory
A;Reference number: A30976; MUID:89136947
A;Accession: A30976
                                                                                                                                                                                                                                                                                                                       A;Reference number: A41403; MUID:90114187
A;Accession: A41403
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R;Nguyen, T.T.; Lazure, C.; Babinski
Mol. Endocrinol. 3, 1823-1829, 1989
A;Title: Purification and primary st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aldosterone secretion inhibitory factor precursor - bovine 'C;Species: Bos primigenius taurus (cattle) (C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Mar-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: natriuretic peptide A precursor C;Reywords: brain; natriuretic F;1-25/Domain: signal sequence *status predicted <SIG>F;26-131/Product: brain gamma natriuretic factor *status predicted <GAM>F;100-131/Product: brain alpha natriuretic peptide *status experimental F;109-125/Disulfide bonds: *status experimental
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A; Residues: 1-131 <MAE>
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A;Residues: 69-103 <NG2>
C;Superfamily: natriuretic peptide A precursor
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A; Accession: A31517
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70; Conserv
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52.2%;
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Pred. No. 9.9e
21; Mismatches
Score 246.5;
Pred. No. 5.6e
14; Mismatches
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No. 9.9e-25;
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A;Molecule type: DNA
A;Rosidues: 1-14, Vy,16-121 <ROY>
A;Residues: 1-14, Vy,16-121 <ROY>
A;Residues: 1-14, Vy,16-121 <ROY>
A;Residues: Fine Accession: A54893; MUID:9204985; PIDN:AAA41456.1; PID:9204986
A;Coss-references: GB:M60731; NID:9204985; PIDN:AAA41456.1; PID:9204986
A;Note: the authors translated the codon GTT for residue 15 as Leu
R;Thuerauf, D.J.; Hanford, D.S.; Glembotski, C.C.
J. Biol. Chem. 269, 17772-17775, 1994
A;Title: Regulation of rat brain natriuretic peptide transcription. A potential A;Reference number: A54893; MUID:94299479
A;Accession: A54893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                brain natriuretic factor precursor - rat
N;Alternate names: brain natriuretic peptide; cardiac natriuretic factor; iso-atrial na
N;Alternate names: brain natriuretic factor BNP-45
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A30162; A3591; A54893; A32918; A32919; A33253; A60735; I57704; A33252
C;Accession: A30162; A3591; A54893; A35918; A35919; A33253; A60735; I57704; A33252
R;Kojima, M.; Minamino, N.; Matsuo, H.
Biochem. Biophys. Res. Commun. 159, 1420-1426, 1989
A;Title: Cloning and sequence analysis of cDNA encoding a precursor for rat brain natri
A; Reference number: A30162; MUID:89193742
A;Cross-references: GB:U02972; NID:g458021; PIDN:AAA21648.1; R;Aburaya, M.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, F Biochem. Biophys. Res. Commun. 163, 226-232, 1989
A;Title: Isolation and identification of rat brain natriureti A;Reference number: A32918; MUID:89374230
                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 171, 416-423, 1990 A; Title: Organization of the gene for iso-rANP, a A; Reference number: A35691; MUID:90365739
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R;Seilhamer, J.J.; Arfsten, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.! Biochem. Biophys. Res. Commun. 165, 650-658, 1989
A;Title: Human and canine gene homologs of porcine brain natriuretic peptide A;Reference number: A36736; MUID:90088474
A;Accession: B36736
                                                                                                                            A; Molecule type: DNA
A; Residues: 1-19 <THU>
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A; Residues: 1-121 <KOJ>
A; Residues: 1-121 <KOJ>
A; Cross-references: GB:M25297; NID:g602483;
R; Roy, R.N.; Flynn, T.G.
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C;Superfamily: natriuretic peptide
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Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Dec-1994
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Pred. No. 6.
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                          peptides in
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Riogawa, Y.; Iton, H.; 1921, 1994
J. Clin. Invest. 93, 1911-1921, 1994
A;Title: Molecular cloning of the complementary
Therence number: 149548; MUID:94237953
                                                                                                           brain natriuretic peptide - mouse.

C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I49548
C;Accession: I49548
C;Accession: Itoh, H.; Tamura, N.; Suga, S.; Yoshimasa, T.; Uehira, M.; Mat
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A; Residues: 77-119, 'Q', '121 <FLY>
R; Nakao, K.; Itoh, H.; Kambayashi, Y.; Hosoda, K.;
Hypertension 15, 774-778, 1990
A; Title: Rat brain natriuretic peptide. Isolation
A; Reference number: A60735; MUID:90277148
A; Accession: A60735
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A;Molecule type: DNA
A;Residues: 1-121 <RES>
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A; Residues: 77-121 <NAK>
R; Dagglino, L; Drouin, J; Nemer, M.
R; Dagglino, L; Drouin, J; Nemer, M.
Mol. Endocrinol. 5, 1292-1300, 1991
A; Title: Differential expression of natriuretic A; Reference number: 157704, MUID: 92123224
A; Accession: 157704
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A; Residues: 77-121 < KAM>
R; FEIJun, T.G.; Brar, A.; Tremblay, L.; Sarda, I.;
Biochem. Biophys. Res. Commun. 161, 830-837, 1989
A; Title: Isolation and characterization of iso-ran
A; Reference number: A33253; MUID:89286593
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A; Title: Isolation and sequence determination of a
A; Reference number: A32919; MUID:89374231
A; Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 1.1e
18; Mismatches
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A;Gene: BNP
A;Introns: 42/3
C;Superfamily:
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A;Cross-references:
C;Genetics:
                                         alpha-atrial natriuretic peptide precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #: C;Accession: S14320; A31509 R;Akizuki, N.; Kangawa, K.; Minamino, N.; Matsuo, H. FEBS Lett. 280, 357-362, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:S58667; NID:g299794; PIDN:AAB26344.1; PID:g299795 A;Experimental source: BALB/c A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:130161, NCBIP:13016; C;Superfamily: natriuretic peptide A precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
A49144
A; TITLE: Cloning and sequence analysis of A; Reference number: S14320; MUID:91192169
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A; Residues: 1-121 <STE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type-B natriuretic peptide, BNP - mouse C; Species: Mus musculus (house mouse) C; Date: 19-Dec-1993 #sequence_revision
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irc. Res. 72, 984-992, 1993
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Pred. No. 5e-09;
5; Mismatches
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A;Accession: A31509
A;Molecule type: protein
A;Residues: 112-140 <MIY>
C;Superfamily: natriuretic
F;118-134/Disulfide bonds:
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R;Olkawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato, H.; Matsuo, H.
Biochem. Biophys. Res. Commun. 132, 892-899, 1985
A;Title: Structure of dog and rabbit precursors of atrial natriuretic polypeptides
A;Reference number: A90119; MUID:86076957
A;Accession: A25302
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A; Residues: 1-140 <AKID
A; Cross-references: GB:X57702; NID:g63648; PIDN:CAA40879.1; PID:e1334751; PID:g380590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atrial natriuretic peptide precursor - dog N;Alternate names: ANP; atrial natriuretic polypeptide C;Species: Canis lupus familiaris (dog) C;Date: 31-Mar-1988 *sequence_revision 31-Mar-1988 *te
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A; Status: pre
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A; Residues: 1-149 <OIK>
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Matches 43
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114 RALLAAPRS---LRRSSCFGGRMDRIGAQSGLGCNSFR 148
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                                                                                                EQNAEAGAALSPLPEVPPWTGEVSPAQRDGGALGRSPWDSSD--
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43; Conser
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Pred. No. 0.00018;
5; Mismatches 44
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C:Species: Homo sapiens (man)
C:Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 18-Jun-1999
C:Accession: A23693; B23693; A01424; B29370; A32733; I58054; S14097; I39458; R:Nemer, M.; Chamberland, M.; Sirois, D.; Argentin, S.; Drouin, J.; Dixon, R Nature 312, 654-656, 1984
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                                                                                                 A;Residues: 1-151,'RR' <NE2>
A;Note: allelic variant with UGA termination of R;Olkawa, S:; Imai, M.; Ueno, A.; Tanaka, S:;
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A;Accession: A93049
A;Molecula ****
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A;Reference number: A22693;
A;Accession: A22693
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A;Title: Purification and sequence determinates
                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-151, 'RR'
                                                                                                                                                                                                        A; MoLecule type: DNA
A; Residues: 1-151 <NEM>
A; Cross-references: GB:X01470;
A; Accession: B22693
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C; Superfamily: natrium
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A; Residues: 1-152 < VLA>
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                                                                                  Nature 309,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;129-145/Disulfide bonds: #status predicted
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S:; Imal, 1914
19, 724-726, 1984
Cloning and sequence analysis of
Cloning and sequence analysis of
number: A01424; MUID:84219799
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                                                                                                                                                                                                                                                                                                                              of human cardiac hormone 593; MUID:85061626
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Pred. No. 0.00
20; Mismatches
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                                                                                                      codon replaced
; Noguchi, T.; N
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Nakazato, H.; Kangawa,
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R. Makayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi, S. Nature 310, 699-701, 1984

A.; Pittle: mRNA sequence for human cardiodilatin-atrial natriuretic factor A.; Reference number: I58054; MUID:84295577

A.; Accession: I58054
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: I19-151, 'RR' <RE2>
A;Cross-references: GB:K02044; NID:g178631; PIDN:AAA51730.1; PID:g178632
R;Maki, M.; Parmentier, M.; Inagami, T.
Blochem. Blophys. Res. Commun. 125, 797-802, 1984
A;Title: Cloning of genomic DNA for human atrial natriuretic factor.
A;Reference number: I39459; MUID:85096983
A;Accession: I39459
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A; Title: Hydrolysis of intact and Cys-Phe-cleaved A; Reference number: S14097; MUID:91176998
A; Accession: S14097
                                                                                                                                                                   R:Greenberg, B.D.; Bencen, G.H.; Seilhamer, J.J.; Nature 312, 656-658, 1984
A;Title: Nucleotide sequence of the gene encoding A;Reference number: 137167; MUID:85061627
A;Accession: 137167
                                                                                                                                                                                                                                            A;Status: Line: DNA
A;Rolecule type: DNA
A;Residues: 1-64,'D',66-151 <RE4>
A;Residues: 1-64,'D',66-151 <RE4>
A;Cross-references: GB:M54951; NID:g178636; PIDN:AAA35529.1; PID:g178638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:K02399; NID:g178633; PIDN:AAA35528.1; PID:g178634
R;Seidman, C.E.; Bloch, K.D.; Zisfein, J.; Smit, J.; Haber, E.; Homcy, C.
Hypertension 7, 31-34, 1985
A;Title: Molecular studies of the atrial natriuretic factor gene.
A;Reference number: I39460
A;Accession: I39460
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A; Residues: 124-151 (YANN)
A; Residues: 124-151 (YANN)
A; Note: natural and synthetic peptide sujected to kallikrein proteolysis
R; Zivin, R.A.; Condra, J.H.; Dixon, R.A.; Seidah, N.G.; Chretien, M.; Nen
Proc. Natl. Acad. Sci. U.S.A. 81, 6325-6329, 1984
A; Title: Molecular cloning and characterization of DNA sequences encoding
A; Reference number: 139458; MUID:85038509
A; Accession: 139458
                                                             A; Molecule type: DNA
A; Residues: 26-151 < RE5>
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Biochem. Biophys. Res. Commun. 118, 131-139, 1
A;Title: Purification and complete amino acid
A;Reference number: A32733; MUID:84128019
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A;Residües: 1-151 <OIK>
A;Cross-references: GB:K02043; NID:g178629; PIDN:AAB59379.1; PID:g178630
R;Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.; Seidman, J.G.
Science 226, 1206-1209, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-75 < RE3>
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A; Residues: 1-151 <RES>
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A; Residues: 1-64, 'D', 66-151 <SEI>
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A; Molecule type: mRNA
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Cross-references: EMBL:X01471; NID:g28690;Comment: Cardiodilantin is a vasoconstric
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atrial natriuretic peptide precursor - horse C; Species: Equus caballus (domestic horse) C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1 C;Accession: S14873
R;Maegert, H.J; Hanke, M.; Schmeding, G.; Teut submitted to the EMBL Data Library, March 1991 A;Reference number: S14872
A;Accession: S14873
A;Status: preliminary
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A;Genetics:
A;Genes: GDB:118727; OMIM:108780
A;Cross-references: GDB:118727; OMIM:108780
A;Cross-references: GDB:118727; OMIM:108780
A;Map position: 1p36-1p36
C;Superfamily: natrium; diuretic peptide A precursor
C;Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-151/Product: cardiodilantin #status predicted <CDD>
F;124-151/Product: atrial alpha natriuretic peptide #status experimental <ANP>
F;130-146/Disulfide bonds: #status experimental
                 atrial natriuretic peptide precursor - pig
N;Contains: alpha atrial natriuretic peptide; gamma atrial natri
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Nov-1993 #sequence_revision 14-Jul-1994 #text_change
C;Accession: S13107; A60899
R;Maegert, H.J.; Appelhans, H.; Gassen, H.G.; Forssmann, W.G.
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C;Superfamily: natriuretic peptide A precursor
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A; Residues: 1-153 <MAE>
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;. 18, 6704, 1990
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6; Mismatches 42
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Search completed: April Job time: 6283 sec

27,

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A; Cross references: EMBL:X54669; NID:g1883; PIDN:CAA38480.1; PID:g1884
R; Forssmann, W.G.; Hock, D.; Lottspeich, A.; Henschen, A.; Kreye, V.; Cl
Anat. Embryol. 168, 307-313, 1983
A; Title: The right auricle of the heart is an endocrine organ. Cardiodil
A; Reference number: A60899
A; Accession: A60899
A; Accession: A60899
A; Residues: 25-54 <FOR>
C; Superfamily: natriuretic peptide A precursor
C; Superfamily: natrium; diuretic; hormone; natriuretic; osmoregulation
F; 124-Domain: signal sequence #status predicted <SIG>
F; 129-150/Product: gamma atrial natriuretic factor #status predicted <ANI
F; 129-145/Disulfide bonds: #status predicted <ANI
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A; Title: Chemical synthesis and cloning of the por A; Reference number: JC1081
A; Mccession: JC1081
A; Mccession: JC1081
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A; Reference number:
A; Accession: S13107
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 16-Feb-1997
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Page

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## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2000, 18:29:24; Search time 8.53 Seconds (without alignments) 469.155 Million cell updates/sec

Title: Perfect score: Sequence:

Scoring table: PEP1 690 1 mdpgtapsrallllf1hla.....rkmdrissssglgckvlrrh 134 BLOSUM62 Gapop 10.0 , Gapext 0.5

searched: 82229 segs, 29864866 residues 82229

lal number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : SwissProt\_38:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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01-MAR-1989 (Rel. 1
01-OCT-1996 (Rel. 3
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SEQUENCE OF 26-131.
MEDLINE; 89061743.
MEDLINE; 89061743.
MINAMINO N., KANGAWA K., MATSUO H.;
"Isolation and identification of a high molecular weight
"Isolation peptide in porcine cardiac atrium.";
natriuretic peptide in porcine (ardiac atrium.")
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Sus scrofa (Pig).
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MEDLINE; 89214071.

PORTER J.G., ARFSTEN A., PALISI T.,

PORTER J.A., SEILHAMER J.J.;

"Cloning of a cDNA encoding porcine
J. Biol. Chem. 264:6689-6692(1989).
                                                                                                                                                                                                                                                                                                                                                                                                          MAEKAWA K., SUDOH T., F
NAKANISHI S., MATSUO H.
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Biophys. Res. Commun. 157:410-416(1988)
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Best Local S
Matches 71
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EMBL; M25547; AAA31007.1; -.
PIR; A31675; A31675.
PIR; A31676, A31676.
PIR; A31517; A31651.
PIR; A316373; A33673.
PIR; S06359; S06359.
                                                                                                                                                                                                                                                           Vasoactive;
SIGNAL
CHAIN
                                                                                                                                                                                               PEPTIDE
PEPTIDE
DISULFID
VARIANT
SEQUENCE
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MEDLINE; 88339957.

SUDOH T., MINAMINO N., KANGAWA K., MATSUO H.;

"Brain natriuretic peptide-32: N-terminal six amino acid
form of brain natriuretic peptide identified in porcine b
Biochem. Biophys. Res. Commun. 155:726-732(1988).

[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EUROpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE: 92007873.

CRAIK D., MUNRO S., NIELSEN K., SHEI THE CONFORMATION OF POTCLINE-brain in dimensional NMR spectroscopy.";

EUR. J. Biochem. 201:183-191(1991).

-I- FUNCTION: VASOACTIVE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INOOKA H., KIKUCHI T., ENDO S., ISHIBASHI Y., WAKIMASU M. "Conformation in solution of porcine brain natriuretic pedetermined by combined use of nuclear magnetic resonance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUDOH T. KANGAWA K., MINAMINO
"A new natriuretic peptide in posture 332:78-81(1988).
[6]
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MEDLINE; 88156915.
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121 ssssglgckvlrrh
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LEVELS THAN ANP.
SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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| MGPRMALPR-VLLLLFLHLLLLGCRSHPLGGAGLASEL--PGIQELLDRLRDRVSELQAE
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                                               RTDLEPLRQDRGLTEAWEAREAAPTGVLGPRSSIFQVLRGIRSPKTMRDSGCFGRRLDRI
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131
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132
125
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Pred. No. 1.5e
(0) Mismatches
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BRAIN NATRIURETIC PEPTIDE
BRAIN NATRIURETIC PEPTIDE
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Matches
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ANFB_BOVIN
P13204;
01-JAN-1990
01-DEC-1992
01-OCT-1996
                                                             BOVIN
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide. ";
Biochem. Biophys. Res. Commun. 165:650-658(1989)
-!- FUNCTION: VASOACTIVE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITIE: 90088474.
SEILHAMER J.J., ARFSTEN A., MILLER J.A.,
SCARBOROUGH R.M., LEWICKI J.A., PORTER J.
SCARBOROUGH RAMINE gene homologs of porcir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CANFA
                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M31777; AAA30832.1; -. PIR; B36736; B36736.
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Eukaryota; Metazoa; Chordata; Cr
Eutheria; Carnivora; Fissipedia;
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                                                                                                                             cfgrkmdrissssglgckvlrrh 134
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                                                                                                                                                                                                                              mdpqtapsralllllflhlaflggrshplgspgsasdl----etsgl---qeqrnhlqgk 53
                                                                                                                                                                              CFGRRLDRIGSLSGLGCNVLRKY
                                                                                                                                                                 VSELQAEQLALEPLHRSHSPA---
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27
107
112
118
140
(Rel. 13, Created)
(Rel. 24, Last sequence update)
(Rel. 34, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                       Brain;
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50.3%;
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Pred. No. 8
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BRAIN NATRIURETIC PEPTIDE (BNP-34).
BRAIN NATRIURETIC PEPTIDE (BNP-29).
BY SIMILARITY.
; DCEBCC52 CRC32;
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ia; Canidae; Canis.
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                                                 PRT;
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Best Local Similarity
Matches 53; Conserv
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01-JAN-1990 (Rel. :
01-FEB-1991 (Rel. :
01-OCT-1996 (Rel. :
BRAIN NATRIURETIC !
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DISULFID
SEQUENCE
                                            SEQUENCE FROM N.A.
MEDLINE; 89193742.
KOJIMA M., MINAMINO N., KANGAWA
"Cloning and sequence analysis
brain natriuretic peptide.";
                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bovine chromaffin cells.";
Endocrinology 124:1591-1593(1989).
-!- FUNCTION: INHIBITS ALDOSTERONE SECRETION.
-!- FUNCTION: VASOACTIVE ACTIVITY.
-!- TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCLEVELS THAN ANP.
-!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGUYEN T.T., LAZURE C., BABINSKI K., CHRETIEN M., DE LEAN A., ON "Purification and primary structure of pro-aldosterone secretion inhibitory factor from bovine adrenal chromaffin cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia; I
                                    Biochem.
                                                                                                                                                                  PEPTIDE)
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MEDLINE; 89136947.
NGUYEN T.T., LAZURE C., BABINSKI K.,
"Aldosterone secretion inhibitory fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRAIN NATRIURETIC PEPTIDE INHIBITORY FACTOR) (ASIF).
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SEQUENCE FROM N.A. MEDLINE; 90365739.
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                                                                                                                                                                  (ISO-ANP).
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                                 Biophys.
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                                  Res. Com
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17, Last sequence update)
34, Last annotation update)
PEPTIDE PRECURSOR (BNP) (5
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                                    Commun.
                                                                      KANGAWA
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ALDOSTERONE SECRETION INHIBITORY FACTOR
BRAIN NATRIURETIC PEPTIDE (BNP-26).
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                                                                                                                                                                                                                                         PRT;
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                                  159:1420-1426(1989)
                                                         cDNA encoding
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                                                                                                                                                                                KD CARDIAC NATRIURETIC
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neuropeptide
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"Isolation and identification cardiac atrium.";
Biochem pi---
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                           PEPTIDE
PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAGNINO L., DROUIN J., NEMER M.; "Differential expression of natriuretic extracardiac tissues.";
                                                                                                                                                                            PIR;
                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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MEDLINE; 89374230.
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 DISULFID
                                                     Vasoactive;
SIGNAL
                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 16-
                                                                                                                                                                                                                                                                                                                                                                                                      "Occurrence of a novel cardiac natriuretic peptide in rats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                MUKOYAMA M., ARAI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLYNN T.G., BRAR A., TREMBLAY L., 9 "Isolation and characterization of peptide from rat atria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAMBAYASHI Y., NAKAO K., ITOH H., HOSODA K., SAITO Y., YAMADA T. MUKOYAMA M., ARAI H., SHIRIKAMI G., SGA.-I., OGAWA Y., JOUGASAKI M., MINAMINO N., KANGAWA K., MATSUO H., INOUYE K., IMU; "Isolation and sequence determination of rat cardiac natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 89374231.
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NE; M60731; AAA41455.1;

N60265; AAA41455.1;

N30162; AA0162.

N30162; A30162;

N32918; A32918.

N32918; A32919.
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                                                                                  PF00212; ANP;
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89286579.
NAKAO K., KAMBAYASHI Y., HOSODA K., SAITO Y., YAMADA, NAKAO K., KAMBAYASHI G., SUGA S.-I., YOSHIDA I., II.
                                                                                            PS00263; NATRIURETIC_PEPTIDE;
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            GAMMA-BRAIN NATRIURETIC PEPTIDE.
BRAIN NATRIURETIC PEPTIDE (5 KD CARDIAC NATRIURETIC PEPTIDE) (BNP-45).
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                                                                                                                                                                                                                                                                                There are no rest
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                                                                                                                                                                                                                                                                                                                       "Structure, expression, and genomic mapping of the mouse natrepeptide type-B gene.";
peptide type-B gene.";
Circ. Res. 72:984-992(1993).
-i- FUNCTION: ACTS AS A CARDIAC HORMONE WITH A VARIETY OF BIC ACTIONS INCLUDING NATRIURESIS, DIURESIS, VASORELAXATION, DIURESIS, VASORELAXATION, DIURESIS, VASORELAXATION, DIURESIS, VASORELAXATION, DIURESIS, VASORELAXATION, ACTIONE SECRETION. IT IS THOUGHT OF RENIN AND ACTION ACTION AND ACTION ACTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OGAWA Y., TIOH H., TAMURA N., SUGA S., YOSHIMASA T., UEHIRA M.,
MATSUDA S., SHIONO S., NISHIMOTO H., NAKAO K.;
Molecular cloning of the complementary DNA and gene that encode
mouse brain natriurettc peptide and generation of transgenic mice
that overexpress the brain natriurettc peptide gene.";
J. Clin. Invest. 93:1911-1921(1994).
                                                                                 between the Swiss Institute of Bioinformat. the European Bioinformatics Institute. These by non-profit institutions as long woodified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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OGAWA Y., ITOH H.,
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-HEART;
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Mus musculus (Mouse).
Chordata;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation updat
BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP).
                    EMBL; D16497; BAA03948.1; EMBL; S58667; CAB31712.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB,
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Eutheria; Rodentia;
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SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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Matches 52
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01-MAR-1992 (Rel. 21
01-OCT-1996 (Rel. 34
ATRIAL NATRIURETIC E
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phasi
                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics.
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                                                                                                                                                                                                                                                                                                                                            AKIZUKI N., KANGAWA K., MINAMINO N., MATSUO "Cloning and sequence analysis of complement precursor for chicken natriuretic peptide."
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 91192169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1992 (Rel. 21, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN).
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                                                                                                                                                                                                                                                                                                       SEQUENCE OF 112-140
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                                                                                                                   SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                        Chem. Biophys. Res. Commun. 155:1330-1337(1988).
FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY I KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHICK
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                                                                                                                                   ATRIOPEPTINS
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                                                                                                                                                                                                                                              KANGAWA K., MATSUO H.; -amino acid natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                    Phasianidae;
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Pred. No. 2.
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GAMMA-BRAIN NATRIURETIC PEPTIDE.

BRAIN NATRIURETIC PEPTIDE.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Archosauria; Aves;
lanidae; Phasianinae; Gallus.
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-> L (IN REF. 2).
5548E822 CRC32;
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                                                                         EMBL outstation
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                                                                                       collaboration
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RESULT 8
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Best Local s
Matches 43
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                                                                                                                                                                                                                                                                OIKAMA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.;
"Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned CDNA.";
Biochem. Biophys. Res. Commun. 132:892-899(1985).
-!- FUNCTION: ATRIAL NATRIJERIC FACTOR (AME) IS A POTENT VASOACTIVE
SUBSTRACE SYNTHSSIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY I
                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
Canis familiaris (Dog).
Therents: Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN).
                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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                                                                            EMBL; M12045; AAA30828.1;
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PIR; A31509; A31509.
                                     PFAM; PF00212; ANP;
                                                  PIR; A25302;
PROSITE; PSO
                                                                                                                                                         the European Bioinformatics Institute.
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SIGNAL 1
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                         /asoactive;
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                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                        MISCELLANEOUS: A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF
                                                                                                                                                                                                                           ATRIOPEPTINS.
                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                  PS00263; NATRIURETIC_PEPTIDE;
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118
140 AA;
                       Signal.
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Pred. No. 1.5e
29; Mismatches
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ia; Canidae; Canis.
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PEPTIDE

ATRIAL NATRIURETIC

PEPTIDE,

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RESULT 9
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Best Local Similarity
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SEQUENCE
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                               Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1988 (Rel. 07, Created)
01-MARR-1989 (Rel. 10, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                Vasoactive; Signal.
SIGNAL 1
                                                                                       EMBL; M13145; AAA30375.1;
                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 123-150. MEDLINE; 86173941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure and analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 86215205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovinae; Bos.
                                             PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 136:396-403(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ANP) (PREPRONATRIODILATIN).
   PEPTIDE
                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                        "Purification and sequence determination of bovine atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                          tactor.
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                                                                                                                                                                                                                                                      MISCELLANEOUS: A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
                                                                                                                                                                                                                                                                                               FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                             Sci. 38:1309-1315(1986).
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                                                          PS00263; NATRIURETIC_PEPTIDE;
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Pred. No. 0.
   ATRIAL NATRIURETIC PEPTIDE, ALPHA
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bovine atrial natriuretic
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14 llflhlaflg-grshplgspgsasdletsglgeqrnhlggkl---

LLFLAFQLQGQTRANPV--YGSVSNGDLMDFKNLLDRLEDKMPLEDEVMPPQVLSDQSEE

Matches

Similarity

Conservative

20;

Mismatches

42;

Indels

48;

7;

selqv Gaps

59

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RESULT 10
ANF_HORSE
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Query Match
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                                                             DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ADAMITICUS; TISSUE-HEART ATRIUM;
MAEGERT H.J., RICHTER R., SCHMAEDING G., FORSSMANN W.G.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY & KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ANP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANF_HORSE STANDARD; PRT; 153 AA.

P27104;

P27104;

01-AUG-1992 (Rel. 23, Created)

01-AUG-1992 (Rel. 23, Last sequence update)

01-OCT-1996 (Rel. 34, Last annotation update)

ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                         PIR; S14873; S148
PROSITE; PS00263;
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                                                                                                              SIGNAL
                                                                                                                             Vasoactive;
                                                                                                                                             PFAM; PF00212; ANP;
                                                                                                                                                                                          EMBL; X58563; CAA41443.1; -.
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                                                                                                PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                   ACTIVITY.
MISCELLANEOUS: A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY
                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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47; Conser
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152 ,
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130
                                                                                                                             Signal
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                                                               AA;
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                                                                                                                                                            NATRIURETIC_PEPTIDE;
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16518 MW;
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29.6%;
16.4%;
28.1%;
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Score 113; DB 1;
Pred. No. 0.00033
                                                            ATRIAL NATRIURETIC
BY SIMILARITY.
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                Length 153
                                                                                                PEPTIDE, ALPHA (ANP).
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MBL outstation -
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"Gene structure of human cardiac hormone pronatriodilatin.";
Nature 312:654-656.
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Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Ver

Eukaryota; Primates; Catarrhini; Hominidae;
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SEQUENCE OF 118-153 FROM N.A.

MEDLINE; 85038509.

ZIVIN R.A., CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRET

ZIVIN R.A., CONDRA J.H., DROUIN J.;

"MOLECULAR CIONING and Characterization of DNA sequences
and human atrial natriuretic factors.";

Proc. Natl. Acad. Sci. U.S.A. 81:6325-6329(1984).
                                                                                                                                                                                  MEDLINE; 85065766.
SEIDMAN C.E., BLOCH K.D., KLEIN K.,
"Nucleotide sequences of the human
                                                                                                                                                                                                                                      ractor precursor."; Nature 312:656-658(1984).
                                                                                                                                                                                                            SEQUENCE OF 1-151 FROM N.A. MEDLINE; 85065766.
                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-151 FROM N.A. MEDLINE; 85061627.
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NPPA OR PND.
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13-AUG-1987 (Rel. 05, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC
                                                                                                                      ERRINGTON
                                                                                                                                  SEQUENCE OF
                                                                                                                                                           Science
                                                                                                                                                                                                                                                                             "Nucleotide sequence
                                                                                                                                                                                                                                                                                         FIDDES J.C.;
                                                                                                                                                                                                                                                                                                      GREENBERG B.D., BENCEN G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-151 FROM N.A. MEDLINE; 84295577.
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d mouse atrial natric
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                                                                                                                                                                                    EIDMAN J.G.;
natriuretic
                                                    CHRETIEN
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Matches 47
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PEPTIDE
DISULFID
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EMBL; X02558; CAA25699.1; JOINED.
EMBL; K02043; AAB59379.1; -.
EMBL; X01471; CAA25700.1; ALT_SEQ.
EMBL; K02044; AAA51730.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as a modified and this statement is not removed. Usentities requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Solution conformation of an atrial natriuretic peptide variant selective for the type A receptor."; Biochemistry 33:8897-8904(1994).

-I- FUNCTION: ATRIAL NATRURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY & KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
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SEQUENCE
MEDLINE;
MAKI M.;
"Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Purification and complete amino acid sequence natriuretic polypeptide (alpha-hANP)."; Biochem. Biophys. Res. Commun. 118:131-139(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M30262; AAA35669.
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MEDLINE; 84128019.
                                                                                                                                                                                                                                            SEQUENCE
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SIGNAL
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MISCELLANEOUS: THE HUMAN GENOME CONTAINS 2 DIFFERENT PREPRONATRIODILATIN GENES ONE CODES FOR 2 ARG RESIDUES OF TERMINUS THAT ARE CLEAVED TO FORM THE MATURE PEPTIDE, COTER ENDS IN A TERMINATION CODON IMMEDIATELY AFTER THE OF THE MATURE PEPTIDE.

OF THE MATURE PEPTIDE.

SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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A22693; A22693.
A32733; A32733.
q-tsleplqesprpt
                                                                       llflhlaflg-grshplgspgsasdletsglgeqrnhlggk---
                                           LLLLAFQLLGQTRANPMYNAVSNADL--MDFKNLLDHLEEKMPLEDEVVPPQVLSEPNEE
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Biophys. Res. Co
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85096983.
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                                                                                                                                                                                                                                                                                                                                                                                           Signal;
                                                                                                                                  Conservative
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AAA35669.1; -.
AAA35528.1; -.
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25
55 CARD
151 ATRI.
146 BY S
153 MISS:
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                                                                                                                                                   16.4%;
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A for human atrial natriuretic factor.";
Commun. 125:797-802(1984).
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                                                                                                                                  16;
                                                                                                                              Score 113; DB
Pred. No. 0.00
L6; Mismatches
                                                                                                                                                                                                                                                                                      CARDIODILATIN-RELATED PEFTIDE (CDP).
ATRIAL NATRICKETIC PEFTIDE, ALPHA (ANP).
BY SIMILARITY.
MISSING (IN ONE OF THE TWO GENES).
                                                                                                                                                                                                                                                            MISSING (IN ONE OF /FTId=VAR_000594.
                                                                                                                                                                                                                                              C24A68AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118:131-139(1984)
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                                                                                                                                                     113; DB 1;
No. 0.00033;
gvwksrevategirghrkmvlyt----lr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions ng as its content is in
                                                                                                                                42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
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                                                                                                                                                                          Length 153;
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                                                                                                                                Indels
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Query Match
Best Local S
Matches 50
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P24259;
                                                                        DISULFID
SEQUENCE
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-CCT-1996 (Rel. 34, Last annotation update)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                    PEPTIDE
                                                                                                                                                  Vasoactive;
SIGNAL
                                                                                                                                                                                                                     EMBL; X54669; CAA38480.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HENSCHEN W.G., BIRR C., CARLQUIST M., CHRISTMANN M., FINKE R. MUTT V., REINECKE M.;
"The antrian" - ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPPA.
Sus scrofa (Pig)
                                                                                                                                   PEPTIDE
                                                                                                                                                                           PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiodilatin-126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ANP) (PREPRONATRIODILATIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The auricular myocardiocytes of the heart constitute an endocrine organ. Characterization of a porcine cardiac peptide hormone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-HEART RIGHT ATRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 18:6704-6704(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAEGERT H.J., APPELHANS H.,
"Nucleotide sequence of a po
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                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Res. 238:425-430(1984).
FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF
                                                                                                                                                                                                                                                                                                                                                                               ATRIOPEPTINS
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                                                                                                                                                                          13107; S13107.
6; PS00263; NATRIURETIC_PEPTIDE; 1.
   50;
                Similarity
                                                                      123
129
150 /
                                                                                                                                                               Signal.
   Conservative
                                                                         AA;
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145
16351
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               15.9%;
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                                                                                     CARDIODILATIN RELATED PEPTIDE (CDP)
(BY SIMILARITY).
ATRIAL NATRIUBETIC PEPTIDE, ALPHA (
BY SIMILARITY.
               Score 109.5;
Pred. No. 0.0
                                                                           4FF67B94
    Mismatches
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                .5; DB 1; 0.0007;
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    46;
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                              Length 150;
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                                                                                                      ALPHA (ANP)
   35;
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 Gaps
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ANF_RABIT
                                                                                                                                                  Matches
                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                        DISULFID SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANF_RABIT P07500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OIKAMA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.;
"Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned CDNA.";
Biochem. Biophys. Res. Commun. 132:892-899(1985).
-: FUNCTION: ATRIAL NATRIURALIAN ATRIA AND IS THOUGHT TO PLAY I
SUBSTRACE SYNTHESIZED IN MANMALIAN ATRIA AND IS THOUGHT TO PLAY I
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation updat
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (
                                                                                                                                                                                                                                                                                                                             EMBL; M12046; AAA31162.1; PIR; B25302; AWRB.
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                              PROSITE; PS00263; NATR PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 86076957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPPA.
                                                                                                                                                                                                                                                     PEPTIDE
                                                                                                                                                                                                                                                                                  Vasoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ANP) (PREPRONATRIODILATIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 -- LRRSSCFGGRMDRIGAQSGLGCNSFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATRIOPEPTINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lllllflhlaflg-grshplgspgsasdletsglqeqrnhlqgk-----
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lraprspkmvqgsgcfgrkmdrissssglgckvlr 132
                                                                                          LFCLAFWHPDQIG--ANPVYNAMSNADL--MDFKNLLDHLEDRMPFEDEAVPPQALSEQS
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                                DEAGAALSPLPEVPPWTGEVSPAQRDGEALGRSTWEASE----
                                                         veg-tsleplgesprptg-------vwksrevategirghrkmvlyt----
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                                                                                                                                                  44;
                                                                                                                                                                Similarity
                                                                                                                                                                                                                        124
130
153 AA;
                                                                                                                                                                                                                                                                                  Signal.
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                                                                                                                                                                                                                                                                                                               NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                       25
151 A
146
16843 MW;
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                                                                                                                                                              15.3%;
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                                                                                                                                                  20;
                                                                                                                                                                Score 105.5;
Pred. No. 0.
                                                                                                                                                                                                                                                     ATRIAL NATRIURETIC PEPTIDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                  Mismatches
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(ANF) (ATRIAL NATRIURETIC PEPTIDE)
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                                                                                                                                                                               DB 1;
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                                                                                                                                                    Indels
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                                RSALLKSKLRAL
                                                                                                                                                                                 153;
                                                                                                                                                                                                                                                       ALPHA (ANP).
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119

LTAPRS-

---LRRSSCFGGRIDRIGAQSGLGCNSFR

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RESULT 15
ANF_MOUSE STANDARD;
ID ANF_MOUSE STANDARD;
AC P05125;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last seq.
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Best Local S
Matches 42
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P18909;
                                                                                                                                                                                                                                                                                                                                    PEPTIDE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAKATA J., KANGAWA K., MATSUO H.;
"Identification of new atrial natriuretic peptides in frog heart.";
Biochem. Biophys. Res. Commun. 155:1338-1345(1988).
-I. FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
-I. SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most proposed institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ANP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 89025806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 122-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (XXX-1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           Vasoactive; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990
                                                                                                      118
                                                                                                                              103
                                                                                                                                                         62
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                                                                                                                   spkmvqgsgcfgrkmdrissssg1gc 128
                                                                                                                                                       FAPNYDSADSSNSAPSLTVEAARPGADMMYNRGSWTQQEKSSP----LRNKLRELLNAPR 117
                                                                                                                                                                                                                         ; D01043; BAA00850.1; -. A31510; A31510.
                                                                                                      S--MRRSSDCFGSRIDRIGAQSGMGC 141
                                                                                                                                                                                                          LTFVLLLLALTKVRGGPAYNSPLSSDLSDLKGLLER---LEDRLPVEEVE----TPVQDI 61
                                                                                                                                                                                                                                                                                                                                                                                       PF00212; ANP;
                                                                                                                                                                                                                                                           42;
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                                                                                                                                                                                                                                                                                                                                                                                                   PS00263; NATRIURETIC_PEPTIDE;
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15934 MW;
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  sequence
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Pred. No. 0.0023;
9; Mismatches 4:
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ATRIAL NATRIURETIC
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a; Ranoidea;
                                         PRT;
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                                                                                                                                                                                                                                                                                                                        6A1FA352 CRC32;
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a; Ranidae; |
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                                                                                                                                                                                                                                                                                Length 145;
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Search completed: April Job time: 12259 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eurtheria: Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 85065766.
SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.;
"Nucleotide sequences of the human and mouse atrial natriuretic factor genes.";
Science 226:1206-1209(1984).
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             PIR; A29370; AMMS.
MGD; MGI:97367; NPPA.
PROSITE; PS00268; NATRIURETIC_PEPTIDE;
PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATRIOPEPTINS.
-!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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NPPA OR PND
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ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
118
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                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY .

KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                         raprspkmvqgsgcfgrkmdrissssglgckvlr 132
LA--GPRSLRRSSCFGGRIDRIGAQSGLGCNSFR 149
                                                     ALSE-QTEEAGAALSSLPEVPPWTG--EVNPPLRDGSASRRSPWDPSDRSALLKSKLRAL
                                                                                                                SESITLGEFLVLAFWLPGHIGANPVYSAVSNTDL--MDFKNLLDHLEEKMPVEDEVMPPQ 60
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AURICULIN B (BY SIMILARITY).
ATRIOPEPTIN I (BY SIMILARITY).
ATRIOPEPTIN II (BY SIMILARITY).
BY SIMILARITY.
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Mus.
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Title:
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Listing first 45 summaries
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Maximum DB seq length: 1000000
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21	Result
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30 AA216038 30 AA216138	SUMMARIES
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Fax: 4169785650
Email: lievee
             Contact: Liew CC
Department of Laboratory Medicine and Pathobiology University of Toronto
Banting Institute, 100 College St., Toronto, Ontari
Tel: 4169788758
                                               cDNAs from fetal heart (1996)
Unpublished (1996)
On Sep 12, 1996 this sequence
                                                                                                                                    hp0251.seq.F Human feta
cDNA 5', mRNA sequence.
                                                                                                  Homo sapiens
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                                                                                   Eutheria;
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                                                                                                                      AA216038
AA216038.1 GI:1815985
                                                                           karyota; Metazoa;
theria; Primates;
(bases 1 to 360)
 liewcc@utcc.utoronto
                                                                                                                                      360 bp
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heart, Lambda ZAP Express Homo sapiens
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hp0519.seq.F Human feta
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                                                                                  Department of Laboratory Medicine and Pathobiology University of Toronto
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Seg primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
                                                    Banting Institute, Tel: 4169788758
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On Sep 12, 1996 this sequence
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                                Fax: 4169785650
                                                                                                                              Contact: Liew CC
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/lab_host="E. coli XII-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_
XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor.primer. EcoRI adaptors were ligated, followed digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggaggtagccaccgagggcatccgtgggcacc 271
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BACKWARD:
                                                                                                                                                                     Unpublished (1996)
On May 8, 1995 this sequence version replaced g1:800920
Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                          N85365 500 bp mRNA EST 01-APR-1996
J3336F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA
clone J3336 5' similar to NATRIURETIC PEPTIDE PRECURSOR, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq
                                                                                                           Banting Institute, 100 College St., Tel: 4169788758
                                                                                             Fax: 4169785650
                                                                                                                                            Department of Laboratory Medicine and Pathobiology University of Toronto
                                                                                                                                                                                                                              CDNAS
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                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 500)
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KWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG
primer: 5' GAAATTAACCCTCACTAAAGGG 3'
                                                        il: liewcc@utcc.utoronto.ca
primer: GAAATTAACCCTCACTAAAGGG.
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                                                                                                                                                                                                                             from fetal heart (1996)
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/lab_host="E. coll XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_
XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor primer. EcoRI adaptors were ligated, followed digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

a 126 c 115 g 57 t
/organism="Homo
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/db_xref="taxon:9606"
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Pred. No. 3.4e-54;
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                                                                                                                          Toronto, Ontario,
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                                                                                                      Contact: Liew CC
Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Department of Toronto, Ontar
                                                                                                                                                                                  cDNAs from fetal heart (1996)
Unpublished (1996)
On Sep 12, 1996 this sequence
                                                                                                                                                                                                                                                                                                                                                        AA216173 279 bp
hp0589.seg.F Human feta
cDNA 5', mRNA sequence.
AA216173
           PCR PRIMETS
FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
                                                                                        Fax: 4169785650
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1 (bases 1 to 279)
                                                                           Email: liewcc@utcc.utoronto.ca
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Location/Qualifiers
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/lab_host="E. coli XL1-Blue"
/note="Yector: Lambda ZAP Express; Site_1: EcoRI;
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/clone="J3336"
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92.1%;
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Pred. No. 7e-48;
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wa88a04.x1 NCI_CGAP_GC6
similar to gb:M25296 BRA
                                                                                                                                                                                                       Email: Robert_Strausberg@nlh.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
cDNA_Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
On May 18, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
AI634108
                         CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 425)
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/db_xref="taxon:9606"
/clone_llb="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
/note="Vector: Lambda ZAP Express, Site_1: EcoRI; Site_2:
/note="Vector: Lambda Lambda
.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.7%;
98.1%;
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BRAIN NA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NA EST 26-APR-1999 mo sapiens cDNA clone IMAGE:2303214 3' NATRIURETIC PEPTIDE PRECURSOR (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                         replaced
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                                                                                                                                                                                                              M. Fatima
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-40UP from Gibco

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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcaccacgaagccccaagatggtgcaagggtctggctgtgctttgggaggaagatggaccgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGGAGGTAGCCACCGAGGGCATCCGTGGGCACCGAAAAATGGTCCTCT-CACCCTGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCAGCTCCTCCAGTGGCCTGGGCTGCAAAGTGCTGAGGCGGCAT
                                                                                                                                             Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontar:
Tel: 4169788758
Fax: 4169785650
                                                        PCR PRimers
FORWARD: 5, GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3,
BACKWARD: 5, CCAGTGAATTGTAATACGACTCACTATAGGGCG
BACKWARD: 7, CAAAMMAAACCCTTCACTAAAGGG 3,
                                                                                                                                                                                                                                                              Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1287882.
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Primates; Catarrhini; Hominide
1. (bases 1 to 228)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA216210 228 bp
hp0679.seq.F Human fets
cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                    cDNAs from fetal heart (1996)
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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AA216210.1 GI:1816149
                                                                                                                                                                                                                                                                                                                   Liew,C
                                                                                                                               Email: liewcc@utcc.utoronto.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                  KWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG primer: 5' GAAATTAACCCTCACTAAAGGG 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
/organism="Homo sapiens
                                   Location/Qualifiers
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polylinker; Plasmid DNA from the normalized library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Clone="IMAGE:2303214"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ
/lab_host="DH10B"
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/db_xref="taxon:9606"
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95.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heart,
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Matches 192
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                                                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
On Jun 72, 1998 this sequence version replaced
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1968649 347 bp mRNA EST 25-AUG-1999 wt91b08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514807 3' similar to gb:M25296 BRAIN NATRIURETIC PEPTIDE PRECURSOR (HUMAN);contains element PTR5 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 347)
                                                                                                                                                                                                           CONA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                            www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           numan
                                                                                                                                            primer: -400P from Gibco
                                                                                                                      quality sequence stop: 344.
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/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI: mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."

a 66 c 64 g 43 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2514807"
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:9606"
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Pred. No. 4.9e-30;
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AI186050/c
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Best Local Sim
Matches 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 AGTCCCTCCGTGGGCACCGCAAAATGGTCCTCTACACCCTGCGGGCACCACGAAGCCCCA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 agggcatccgtgggcaccgcaaaatggtcctctacaccctgcgggcaccacgaagcccca 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTGGGCTGCAAAGTGCTGAGGCGGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI186050 356 bp mRNA EST 09-OCT-1998 qe50g02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1742450 3' similar to gb:M25296 BRAIN NATRIURETIC PEPTIDE
                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nlh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 356)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
/lab_host="PDH108"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257095-1258031,
1469044-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo. "
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1742450"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.9%;
98.0%;
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Pred. No. 4.6e-26;
0; Mismatches 3;
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(Pharmacia). Library went through one round

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                 Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 ATCCGTGGGCACCGCAAAATGGTCCTCTACACCCTGCGGGCACCACGAAGCCCCCAAGATG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 atccgtgggcaccgcaaaatggtcctctacaccctgcgggcaccacgaagccccaagatg 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 GTGCAAGGGTCTGGCTTTTGGGAGGAAGATGGACCGGATCAGCTCCTCCAGTGGCCTG
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151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA216011 333 bp
hp0221.seq.F Human fetal
cDNA 5', mRNA sequence.
AA216011
AA216011,1 GI:1815966
                                                                                                                                                                                                                                                                                                                                           PCR PRIMERS
FORWARD: 5' GCCAAGCTGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNAs from fetal heart (1996)
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1324710.
Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 333)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 4169788758
Fax: 4169785650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
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                   Similarity
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 Conservative
                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                     liewcc@utcc.utoronto.ca
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                                                                                                        /db_xref="taxon:9606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XII-Blue"
/note="Yector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor: primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

a 77 c 86 g 87 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W."

83 c 79 g 96 t
                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
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                 34.8%;
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 0
Score 140; DB 30;
Pred. No. 4.8e-25;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heart, Lambda ZAP Express Homo sapiens
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                                      Length 333;
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305 gaagccccaagatggtgcaagggtctggcttgcttttgggaggaagatggaccggatcagct 364

Matches Query Match

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24.4%; ilarity 100.0%; Conservative

Score 98; DB; Pred. No. le-0; Mismatches

DB 49; le-14; 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index (1997) (Inpublished (Inpublishe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI656014 296 bp mRNA EST 04-MAY-1999 tt42e12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2243470 similar to gb:M25296 BRAIN NATRIURETIC PEPTIDE PRECURSOR (HUMPAR 1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40UP from Gibco
Location/Qualifiers
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/TLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria; Primates; 1 (bases 1 to 296)
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AI656014
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National Cancer Institute, Cancer Genome Anatomy
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                                          91
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                         /note="Vector: pf773D-Pac (Pharmacia) with a modified /note="Vector: pf773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 145964-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:2243470"
/clone_lib="NCI_CGAP_GC6"
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/db_xref="taxon:9606"
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AW197593/c
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ORGANISM
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ORIGIN
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                           236
                                            365 cctccagtggcctgggctgcaaagtgctgaggcggcat 402
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                                                                                                                                              gaagccccaagatggtgcaagggtctggctgtgctttggggaggaagatggaccggatcagct 364
                                                                                                                     GAAGCCCCAAGATGGTGCAAGGGTCTGGCTGCTTTGGGAGGAAGATGGACCGGATCAGCT 237
                        CCTCCAGTGGCCTGGGCTGCAAAGTGCTGAGGCGGCAT
                                                                                                                                                                                                                    98;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
On Jul 8, 1999 this sequence version replaced g1:5422539
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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1 (bases 1 to 296)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA
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AW197593
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EST.
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                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled germ cell tumors"
/lab_host="DHIDB"
/lab_host="DHIDB"
/note="Prector: pT7T3D-Pac (Pharmacia) with a modified
/note="Prector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258651,
1469044-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo. "
91 a 72 c 61 g 72 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:2687100"
/clone_lib="NCI_CGAP_GC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                     24.4%;
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                                                                                                                                                                                                                                     Score 98; DB 74;
Pred. No. 1e-14;
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                                                                                                                                                                                                                                                           74; Length 296
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                   RESULT 13
AA799914/c
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AUTHORS
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AI656015/c
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                                                                                                                                              369 cagtggcctgggctgcaaagtgctgaggcggcat 402
                                                                                                                     220 CAATGGCATGGGCTGCACAGTGGTAAGGCGGCAT 187
                                                                                                                                                                                                                 280 CCCAATATGTGTGCAAGGGTCTGTCTGCTTTGGTAGGCAAATGGACCGGATCAGCTCCTC 221
                                                                                                                                                                                                                                                                                                                                    Local
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Unpublished (1997)
On Jun 5, 1998 this sequence version replaced g1:3187757
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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1 (bases 1 to 284)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Mational Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1459064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:2243449"
/clone_lib="NCI_CGAP_GC6"
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/db_xref="taxon:9606"
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Pred. No. 8e-0
0; Mismatches
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Sequencing Center information can be

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M. Fatima Ph.D., Michael

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ORGANISM
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RHEBR49 3' end, mRNA sequence.
AI103777
AI103777.1 GI:3708283
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                                                                   Rattus sp.
Rattus sp.
Rattus sp.
Rattus sp.
Eutheria; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 373)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quacken
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) C
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1 (bases 1 to 337)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (301)-838-3529
Fax: (301)-838-0208
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On Jan 19, 1998 this sequence version
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primer: M13-21.
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/db_xref="ATCC (inhost):2006874"
/db_xref="taxon:10118"
/clone="RHEAG83"
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/note="organ: heart; Vector: pT7T3Pac; for the control of the cont
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             The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized AV canal at 16.5 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 93-136,
                                                                                                                                                                              Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI704051 377 bp mRNA
UI-R-AC1-xq-f-11-0-UI.sl UI-R-AC1 Rattus
UI-R-AC1-xq-f-11-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: nhlee@tigr.org
Seq primer: M13-21.
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Fax: (301)-838-0208
Email: nhlee@tigr.or
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The Institute for Genomic Research
9712, Medical Center Drive, Rockville,
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97044477
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Eutheria; Rodentia;
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>(TAAA)n#Simple_repeat
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/note="Organ: heart; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
84 c 83 g 84 t
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/db_xref="taxon:10118"
/clone="RHEBR49"
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Search completed: April 27, 2000, 22:02:12 Job time: 12444 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.2%; Score 57; DB 50; Length 377; Best Local Similarity 63.5%; Pred. No. 0.00014; Matches 87; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
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/lab_host="PH108 (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
/note-"vector: pT73D-Pac (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ø
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-AC1-xq-f-11-0-UI"
/clone_lib="UI-R-AC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Result
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Perfect score:
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Maximum DB
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     tal number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                      Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*

1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
6: /cgn2_6/ptodata/
7: /cgn2_6/ptodata/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length: 0
length: 1000000
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Match
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402
1 atggatccccagacagcacc.....gcaaagtgctgaggcggcat 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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  US-08-850-910A-44
US-08-850-910A-19
US-08-850-910A-17
US-08-850-910A-17
US-08-850-910A-22
US-08-643-763A-22
US-08-643-763A-22
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US-08-461-95A-22
US-08-461-397A-22
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US-08-147-03-26
US-08-148-27
US-08-148-27
US-08-447-570-26
US-08-447-570-26
US-08-449-700-26
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US-08-499-523-9	US-08-356-060A-4	US-08-176-427B-7	US-08-809-740A-4	US-08-809-740A-1	US-07-757-606B-7	US-07-757-606B-3	US-07-728-221B-12	US-07-757-606B-5	US-07-757-606B-2	5212286-1	5212286-5	PCT-US93-10520-9	PCT-US93-08885-22	PCT-US93-08808-22	PCT-US93-08742-22	PCT-US93-07231-22	PCT-US93-07190-22
Sequence 9, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 3, Appli	Sequence 12, Appl	Sequence 5, Appli	Sequence 2, Appli	Patent No. 5212286	Patent No. 5212286	Sequence 9, Appli	Sequence 22, Appl				

## ALIGNMENTS

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US-08-850-910A-44
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                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2190020:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: 202-887-1500
TELECAX: 202-887-1500
                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1519 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SEILHAMER, J.J.

APPLICANT: LEWICKI, J.

APPLICANT: SCARBOROUGH, R.M.

TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR

TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 5
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CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/850,910A FILING DATE: 05-MAY-1997 CLASSIFICATION: 435
STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08850910A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: MORRISON & FOERSTER, LLP
2000 Pennsylvania Avenue, NW, Suite 5500
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linear
                 single
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COMPUTER REALIZED DISKETCE
MEDIUM TYPE: DISKETCE
MEDIUM TYPE: DISKETCE
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/477,226
FTLING DATE: 08-FEB-1990
FTLING DATE: 08-FEB-1990
FTLING DATE: 08-FEB-1990,880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5948761
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40, Application US/08850910A Patent No. 5948761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 261; Conserv
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SEILHAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491 TTGCAGGAGCAGCGCAACCATTTGCAGGGCAAACTGTCGGAGCTGCAGGTGGAGCAGACA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 ttacaggagcagcgcaaccatttgcagggcaaactgtcggagctgcaggtggagcagaca 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      551 TCCCTGGAGCCCCTCCAGGAGAGCCCCCCGTCCCACAGGTGTCTGGAAGTCCCGGGAGGTA 610
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LOCATION: 1295...1308
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OTHER INFORMATION:
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LOCATION: 497...752
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Pred. No. 2.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                          Suite
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RESULT
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Best Local Similarity 69.6
Matches 279; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 215
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEPAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 707 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/20
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
                                                                                                                                                                                                                                                                        331
                                                                                                                                                                                                         241 gaggtagccaccgagggcatccgtgggcaccgcaaaatggtcctctacaccctgcgggca
                                                                                                                                                                                                                                                          271
                                                                                                                                                                                                                                                                                                                                             121 tocgggttacaggagcagcgcaaccatttgcagggcaaactgtcggaggttgcaggtggag 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 ATGGGCCCCGGGATGGCGCTTCCCCGCGTGCTCCTGCTC---TCTTGCACCTGTTG 156
                                                                      391 ATACGCAGCCCCAAGACGATGCGTGACTCTGGCTGCTTTGGGCGGAGGCTGGACCGGATC
                                                                                                                                                                                                                                                                                                                        214 --- GGGATACAGGAGCTGCTGGACCGCCTGCGAGACAGGGTCTCCGAGCTGCAGGCGGAG
                                                                                                                                                                                                                                                                                                                                                                                           157 CTGCTAGGATGCCGTTCCCATCCACTGGGTGGCGTGGCCTGGCCTCAGAACTGCCA---
                                                   451 GGCTCCCTCAGCGGCCTGGGCTGCAATGTGCTCAGGAGGTA 491
                                                                                                                                                    301 ccacgaagccccaagatggtgcaagggtctggctgctttgggaggaagatggaccggatc
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LOCATION: 100...492
OTHER INFORMATION:
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 182.2; DB 4
Pred. No. 1.8e-40;
0; Mismatches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 707;
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                                                                                                                                                       360
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                                                                                                                       450
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RESULT

S-08-850-910A-38

US-08-850-910A-38

Sequence 38, Application US/08850910A

Patent No. 5948761

PATECANT: SEILHAMER, J.J.

APPLICANT: LEWICKI, J.

APPLICANT: LEWICKI, J.

APPLICANT: CEARBOROUGH, R.M.

TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR

TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER, LLP

STREET: 2000 Pennsylvania Avenue, NW, Suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299
FILING DATE: 19-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/850,910A
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 469...723
OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: 1281...1292
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20006-1888
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                            646
                                                                                                                                                                                        526
                                                                                                                                                                                                                                                                        130 caggagcagcgcaaccatttgcagggcaaaactgtcggagctgcaggtggagcagacatcc 189
706
                                                                                                                                                        250
                                                                                                                                                                                                                     190
                                                                                                                                                                                                                                                   Local Similarity 71.0 nes 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1507 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 100...2
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/206,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                agtggcctgggctgcaaag 388
                                                                             cccaagatggtgcaagggtctggctttgggaggaagatggaccggatcagctcctcc 369
                                                                                                                                          accyayygcatccytyyycaccycaaaatyytcctctacaccctycyyygcaccacyaayc 309
                                                                                                                                                                                                        ctggagcccttccaggagagcccccgtcccacaggtgtctggaagtcccgggaggtagcc 249
                                                           CCCAAGACGATGCGTGACTCTGGCTGCTTTGGGCGGAGGCTGGACCGGATCGGCTCCCTC 705
                                                                                                                       CCCACGGGGTTCTTGGGCCCCGCAGTAGCATCTTCCAAGTCCTCCGGGGAATACGCAGC 645
                                                                                                                                                                                      CTGGAGCCCCTCCGGCAGGACCGTGGCCTCACAGAAGCCTGGGAAGCCAAGGCAAGCAGCC 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100...222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                             34.6%;
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                                                                                                                                                                                                                                                                                                              Score 139; DB 4; Pred. No. 8.3e-29; O; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219002025212
                                                                                                                                                                                                                                                                                                                                             Length 1507;
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RESULT 4 US-08-850-910A-17

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                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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OPERATING SYSTEM: Windows
OPERATING SYSTEM: Windows
OPERATING SYSTEM: Windows Version 2.4
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/850,910A
FILING DATE: 05-MAY-1997
435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: SEILHAMER,
APPLICANT: LEWICKI, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/477,226
FILING DATE: 08 FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 11-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE, Kate H
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
310 cccaagatggtgcaagggtctggctttgggagggaaggatggaccggatcagctcctcc
                                                              585
                                                                                                                                                                            190
                                                                                                                                                                                                                  466
                                                                                                                                                                                                                                      130 caggagcagcgcaaccatttgcagggcaaactgtcggagctgcaggtggagcagacatcc 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                          Local Similarity
es 181; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                        CCCACGGGGGTTCTTGGGCCCCGCAGTAGCATCTTCCAAGTCCTCCGGGGAATACGCAGC
                                                                                            accgagggcatccgtgggcaccgcaaaatggtcctctacaccctgcgggcaccacgaagc
                                                                                                                                                                      ctggagcccctccaggagagcccccgtcccacaggtgtctggaagtcccgggaggtagcc 249
                                                                                                                                                                                                                CTGGAGCCCCTCCGGCAGGACCGTGGCCTCACAGAAGCCTGGGAAGGCAAGGCAAGCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202-822-0168
                                                                                                                                                                                                                                                                                          30.8%; ilarity 69.9%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCARBOROUGH, R.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECOMBINANT TECHNIQUES FOR PRODUCTION OF BRAIN NATRIUETIC PEPTIDE 50
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                                                                                                                                                                                                                                                                                        Score 123.8; DB 4;
Pred. No. 9.8e-25;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                          Length 1504;
                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                      584
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US-08-850-910A-42; Sequence 42, Application US/08850910A; Patent No. 5948761
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                                                                                          US-08-850-910A-42
Query Match 29.
Best Local Similarity 67.
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FASTSEQ for Wind CURRING PAPLICATION DATA:
APPLICATION UMBER: US/08/
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/477
FILING DATE: 08-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/29
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200
                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 211
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
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                                                                                                                                    NAME/KEY: CDS
LOCATION: 740...79:
OTHER INFORMATION:
NAME/KEY: CDS
                                                                                                                                                                           NAME/NET 155...
LOCATION: 365...
OTHER INFORMATION:
CDS CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     705 AGCGGCCTGGGCTGCAATG 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2000 Pent
CITY: Washington
                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                     LOCATION: 1558...
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                        ENGTH:
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1558...1569
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                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                        .791
                                                                                                                                                                                                                          .490
                        29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         219002025212
      Score 116.4; DB 4;
Pred. No. 9.9e-23;
0; Mismatches 81;
                                     Length 1804;
          Indels
        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22,
Patent No. 5
                                                                                                                                                        TELEFAX: (508) 435-695
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                                 NAME: PITCHER ESQ., EDMUND R.
PRECISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PatentIn Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0:
FILING DATE: 20-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 agccccaagatggtgcaagggtctggcttgctttgggaggaagatggaccgggatcagctcc 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 247 gccaccgagggcatccgtgggcaccgcaaaatggtcctctacacccttgcggggcaccacga 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    971 CTCAGTGGCCTGGGCTGCAATG 992
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NAME/KEY: CDS
LOCATION: 93..1289
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U:
ZIP: 01748
                                                                                                   TRANDEDNESS:
OPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGCCCCGTGGGGTCCTTGCACCCCATGACAGTGTCCTCCAGGCCCTGAGAAGACTACGC
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                                                                                                                                    nucleic acid
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OZKAYNAK, ENGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RUEGER, DAVID C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART,
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                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                 CDNA
                                                                                                                   single
                                                                                                                                                                                                                 435-6951
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  /product- "MOP2 CDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                               US/08/278,729A
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US-08-480-528A-9/c
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Best Local Similarity 47.9
Matches 145; Conservative
                                                                                                                                                                                                               APPLICATION NUMBER: US/08/480,5
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq., GILLIAN M.
REGISTRATION UMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: 093-INDUCED MORPHOGENESIS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
MOLECULE TYPE:
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                                                        LENGTH: 1926 base pairs TYPE: nucleic acid
                  STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers1
CURRENT APPLICATION NUMBER: US/08/643,563A
FILING DATE: 06-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY ESq., MICHAEL J.
REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: CRP-058CN2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
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Matches
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                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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LOCATION: 93..1289
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 CAAGGCCCAATAGCCAGAGTGGCCCGGGACGCATAGCCATCTCGGACTTTCAGCCGGCGC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 tagccaccgagggcatccgtgggcaccgcaaaatggtcctctacaccctgcgggcaccac 304
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                                                                                                                                                                                                                                                                                                                        STATE:
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OPPERMANN, HEAL
OZRAYNAK, ENGIN
T: KUBERASAMPATH, THANGAVEL
THORGER, DAVID C.
                                                                                                                                                                                                                                                                                                                      MA
                                                                                                                                                                                                                                                                                                                                                         45 SOUTH STREET
                                                                                                                                                                                                                                                                                                     USA
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/product= "mOP2-PP"
/note= "mOP2 cDNA"
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Pred. No. 0.03
0; Mismatches
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                                                                                                                                                                                        Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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LOCATION: 93.1289

COTHER INFORMATION: /:
US-08-643-563A-22
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Best Local Similarity
atches 145; Conserv
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                8-643-763A-22/c
            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/643,763A FILING DATE: 06-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                  uence 22, Application US/08643763A
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             APPLICANT: COHEN, CHARLES M. APPLICANT: PANG, ROY H.L.
                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MORPHOGENIC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 CAAGGCCCAATAGCCAGAGTGGCCCGGGACGCATAGCCATCTCGGACTTTCAGCCGGCGC 73
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                                                                                                                                                                                        CITY: HOPKINTON
STATE: MA
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                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                       STREET:
CLASSIFICATION:
                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATCCACTGGTAGCTGGTCGGGCTCGGCTGACGCCAGACGGGGAGGACCAGACGGCGCA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tagccaccgagggcatccgtgggcaccgcaaaatggtcctctacaccctgcgggcaccac 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGCTGGGGACAGGTGTGCGGGGGACGCGGACCGTGGCCGCCTCCCCAGCGCGCACAGAG 133
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                                                                                                                                                                                                                         45 SOUTH STREET
                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                 RUEGER, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                  KUBERASAMPATH,
                                                                                                                                                                                                                                                                                                                                                               OPPERMANN, HERMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                           PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.98;
                                                                                                                                                                                                                                                                                                               MORPHOGENIC-INDUCED PERIODONTAL TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "MOP2 CDNA"
                                                                                                                                                                                                                                                                                                                                                                                                   THANGAVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39.8; DB 2;
Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157;
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                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/08462623
Patent No. 5739107
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 145; Conserv
                                                                                                                                                                                                                                                                                          GENERAL INFOR APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 248-71
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
VOLECTER
                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pair:
                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                      IITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL IITLE OF INVENTION: ULCERS.
                                                                                                                                                                         APPLICANT:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
COUNTRY: USA
ZIP: 01748
                                 STATE: MA
                                                                   STREET:
                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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                                                HOPKINTON
                                                                  E: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES 45 SOUTH STREET
                                                                                                                                                                                                                                      CHARETTE, MARC F.
KUBERASAMPATH, TH
RUEGER, DAVID C.
                                                                                                                                                                         SMART, JOHN E
                                                                                                                                                                                      OPPERMANN, HERMANN
PANG, ROY H.L.
OZKAYNAK, ENGIN
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Pred. No. 0.033;
0; Mismatches 157;
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RESULY 11
US-08-451-953A-22/c
US-08-451-953A-22/c
Sequence 22, Application US/08451953A
Patent No. 5741641
GENERAL INFORMATION:
APPLICANT: SMART, JOHN
APPLICANT: OZKAYNAK, HERMAN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
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APPLICATION UNBER: US 08/445,882
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-074CN
TELECOMMUNICATION INFORMATION:
TELEPAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.9%; Score 39.8; DB Best Local Similarity 47.9%; Pred. No. 0.033; Matches 145; Conservative 0; Mismatches 1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
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NAME/KEY: CDS
LOCATION: 93..1289
OTHER INFORMATION:
US-08-451-953A-22
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FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER Esq., EDMUND R.
REGISTRATION NUMBER: CRP-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-6951
INFORMATION FOR ESD ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 145; Conservative
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Best Local Similarity
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TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                  245
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                                          365 cct 367
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STRANDEDNESS: sing
TOPOLOGY: linear
12 CCT 10
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                                                                                                                       gaagccccaagatggtgcaagggtctggctgctttgggaggaagatggaccggatcagct 364
                                                                                                                                                                                             tagccaccgagggcatccgtgggcaccgcaaaatggtcctctacacccctgcgggcaccac 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39.8; DB 2;
Pred. No. 0.033;
0; Mismatches 157,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRP-058CN
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RESULT 12 US-08-445-468A-22/c S-08-445-468A-22/c S-8quence 22, Application US/08445468A ; Patent No. 5849686

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi
APPLICATION UNMBER: US/08/445,468A
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
AMME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-072FW2
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 22:
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est Local Similarity 47.9%;
atches 145; Conservative
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APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMANN, HERMAN
APPLICANT: PANG, ROY H. L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                               132
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                                            365 cct 367
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LOCATION: 93..1289
OTHER INFORMATION:
12 CCT 10
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                                                                                                                           gaagccccaagatggtgcaagggtctggctgctttgggaggaagatggaccggatcagct 364
                                                                                                                                                                                                                                                                                                           atccctggagcccctccaggagagcccccgtcccacaggtgtctggaagtcccgggag-g 244
                                                                                        GCATCCACTGGTAGCTGGGCTCGGCCTGACGCCAGACGGGGAGGACCAGACGGCGCA 13
                                                                                                                                                                               CAAGGCCCAATAGCCAGAGTGGCCCGGGACGCATAGCCATCTCGGACTTTCAGCCGGCGC 73
                                                                                                                                                                                                                  tagocacogagggcatcogtgggcacogcaaaatggtcotctacacocctgcgggcaccac 304
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US-08-461-397A-22/c
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; LOCATION: 93..1289
; OTHER INFORMATION:
US-08-461-397A-22
                                                                                                                                                                                                                                                                                                    Query Match 9.9%;
Best Local Similarity 47.9%;
Matches 145; Conservative
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617/248-700
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: COHEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,397A
FILING DATE: 05-UN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITITLE OF INVENTION: PROLIFERATION OF EPITHELIAL NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                     186 atccctggagcccctccaggagagcccccgtcccacaggtgtctggaagtcccgggag-g 244
                                                                                                                                                                                   126 gttacaggagcagcgcaaccatttgcagggcaaactgtcggagctgcaggtggagcagac 185
132 CAAGGCCCAATAGCCAGAGTGGCCCGGGACGCATAGCCCATCTCGGACTTTCAGCCGGCGC
                                                                         192 GACGCTGGGGACAGGTGTGCGGGGGACGCGGACCGTGGCCGCCTCCCAGCGCGCACAGAG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 01748
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TOPOLOGY: lir
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                               tagccaccgagggcatccgtgggcaccgcaaaatggtcctctacaccctgcgggcaccac 304
                                                                                                                                                   GTAGCCCGAGCACCGCCAGGATTTCACGCTGCATGTCGCGGGGGCGCTCGCGCGCTCCCAGGC
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KUBERASAMPATH, THANGAVEL
RUGGER, DAVID C.
OPPERMAN.
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PANG, ROY H.L.
OZKAYNAK, ENGIN
SMART, JOHN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                          DB 4;
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; LOCATION: 93..1289
; OTHER INFORMATION:
US-08-912-088-22
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US-08-912-088-22/c
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Best Local Similarity
Matches 145; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY, AGENT INFORMATION:
NAME: PITCHER ESG., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SWART, JOHN
APPLICANT: OPPERMANN, HERMAN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUGGER, DAVID C.
APPLICANT: RUGGER, DAVID C.
APPLICANT: COMEN, ROY H.L.
APPLICANT: COMEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    FEATURE:
                                           312
126 gttacaggagcagcgcaaccatttgcagggcaaactgtcggagctgcaggtggagcagac 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 cct 367
                                                             66 gggaggtcgttcccacccgctgggcagccccggttcagcctcggacttggaaacgtccgg 125
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1926 base pairs
TYPE: nucleic acid
STRANGEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 GCATCCACTGGTAGCTGGTCGGGCTCGGCTGACGCCAGACGGGGAGGACCAGACGGCGCA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 01748
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                                         GGGGCGCGGACGCTGGCCGGGCAGCCGCGGGTTGTGCACGGGGTCGGGGCCGTCCCG 253
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                                                                                                                       Conservative
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                                                                                                                                       9.98;
47.98;
                                                                                                                                                                                                                                      /product= "MOP2 CDNA"
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                                                                                                                   Score 39.8; DB 4; Length 1926;
Pred. No. 0.033;
0; Mismatches 157; Indels 1
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NAME/KEY: CDS
COCKTION: 93.1289
COCHER INFORMATION: /
OTHER INFORMATION: /
OTHER INFORMATION: /
US-07-901-703-12
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US-07-901-703-12/c
US-07-901-703-12/c
; Sequence 12, Application US/07901703
; Patent No. 5344654
; Patent No. 5344654
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                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-0:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                         TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,70:
FILING DATE: 19920616
                                                                                                                                                          TOPOLOGY: lin
ORIGINAL SOURCE:
ORGANISM: MUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KUBERASAMPATH, TI
APPLICANT: OPPERMANN, HERMAI
APPLICANT: OZAKAYNAK, ENGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED TITLE OF INVENTION: OSTEOGENIC PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 atccctggagcccctccaggagagcccccgtcccacaggtgtctggaagtcccgggag-g 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 gaagccccaagatggtgcaagggtctggctgctttgggaggaagatggaccggatcagct 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 CAAGGCCCAATAGCCAGAGTGGCCCGGGACGCATAGCCATCTCGGACTTTCAGCCGGCGC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 GACGCTGGGGACAGGTGTGCGGGGACGCGGACCGTGGCCGCCTCCCAGCGCGCACAGAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 GTAGCCCGAGCACCGCCAGGATTTCACGCTGCATGTCGCGGGGCTCGCGCGCTCCCCAGGC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 tagccaccgagggcatccgtgggcaccgcaaaatggtcctctacaccctgcgggcaccac 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: EXCHA
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                                                                                                                                         TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                         EMBRYO
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                  /function= "OSTEOGENIC PROTEIN"
/product= "mOP2-PP"
/note= "mOP2 cDNA"
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                                                                                                                                       126 gttacaggagcagcgcaaccatttgcagggcaaactgtcggaggttgcaggtggagcagac 185
                                                                                                                                                                                                               192 GACGCTGGGGACAGGTGTGCGGGGGGACGCGGACCGTGGCCGCCTCCCCAGCGCGCACAGAG 133
                                                                                                                                                                                                                                           186 atccctggagcccctccaggagagcccccgtcccacaggtgtctggaagtcccgggag-g 244
                  365 cct 367
                                                                                          305 gaagccccaagatggtgcaagggtctggctttgggaggaagatggaccggatcagct 364
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12 CCT 10
                                                                 72 GCATCCACTGGTAGCTGGTCGGCTCGGCTGACGCCAGACGGGGGACCAGACGGCGCA 13
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Search completed: April 28, 2000, 00:19:25 Job time: 14557 sec

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Result
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Maximum
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
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        Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB seq
      Score
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1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/

4: /cgn2_6/ptodata/

5: /cgn2_6/ptodata/
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140.971 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/1/1aa/FCTUS9_COMB.pep:*
/cgn2_6/ptodata/1/1aa/FCTUS9_COMB.pep:*
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                    US-08-850-910A-48
US-08-38-558-1
US-08-38-558-1
US-08-850-910A-43
US-08-850-910A-47
US-08-850-910A-47
US-08-850-910A-43
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9512286-3
US-07-778-847-2
US-08-850-910A-18
9512286-3
US-07-778-847-2
US-08-850-910A-18
9512286-3
US-07-778-847-2
US-08-850-910A-18
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Sequence 48, Appl
Sequence 1, Appl
Sequence 39, Appl
Sequence 47, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 57, 
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NATRIUET Suite 55	30 92 13.3 29 1 US-07-754-958-6 31 92 13.3 29 1 US-07-754-947-6 32 87.5 12.7 126 2 US-07-757-606B-1 33 87.5 12.7 126 2 US-07-757-606B-6 34 87 12.6 32 1 US-08-737-927-4 35 87 12.6 32 1 US-08-470-846A-18 37 87 12.6 32 2 US-08-470-846A-18 38 87 12.6 32 2 US-08-12591-2 38 87 12.6 32 5 5449751-1 39 87 12.6 32 5 5449751-1 40 86 12.5 20 2 US-08-850-910A-34 41 82 11.9 22 1 US-07-828-450-10 42 82 11.9 27 1 US-07-828-450-13 43 82 11.9 27 1 US-07-828-450-13 44 82 11.9 27 1 US-07-828-450-13 45 82 11.9 27 1 US-07-828-450-13 46 82 11.9 27 1 US-07-828-450-13 47 82 11.9 27 1 US-07-828-450-13 48 82 11.9 27 1 US-07-828-450-13 49 82 11.9 27 1 US-07-828-450-13 40 81 11.9 27 1 US-07-828-450-13 41 82 11.9 27 1 US-07-828-450-13 42 82 11.9 27 1 US-07-828-450-13 43 82 11.9 27 1 US-07-828-450-13 44 82 11.9 27 1 US-07-828-450-13 45 82 11.9 27 4 PCT-US94-02391-4
ETIC PEPTIDE	Sequence 6, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 18, Appli Sequence 18, Appli Sequence 2, Appli Patent NO. 5449751 Patent NO. 5449751 Sequence 10, Appli Sequence 11, Appli Sequence 13, Appli Sequence 13, Appli Sequence 4, Appli Sequence 4, Appli

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Matches 134; Conservative

Local Similarity

100.0%;

Length 134; Indels

0; Gaps

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; Score 690; DB 2; ; Pred. No. 4.8e-71; 0; Mismatches 0;

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US-08-850-910A-45
                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.C
CURRENT APPLICATION DATA:
APPLICATION UNUBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION DATA:
APPLICATION UNUBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
APPLICATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4 Patent No.
                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SEILHAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 202-887-1500
                     MOLECULE TYPE: FRAGMENT TYPE:
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121 ssssglgckvlrrh 134
                                                                                                                                                                                                                                                                                      NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                           TYPE: amino acid
                                                                 TOPOLOGY:
                                                                                                                                                                                                                       TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
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o. 5948761
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2000 Pennsylvania Avenue, NW, Suite 5500
                                                                 linear
                                            protein
                                                                                    single
                                                                                                                                                                                                                                                                                                             29,959
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RESULT

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TELEFAX: (212) 790-9090

TELEX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEMOTH: 76 amino
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                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-338-558-1
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US-08-338-558-1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,558
FILING DATE: 21-NOV-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 8080-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08338558
Patent No. 5786163
GENERAL INFORMATION:
                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 133; Conserv
                                                                                                                                                Matches
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ssssglgckvlrrh 134
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121 ssssglgckvLRRH 134
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STATE: New York
                             87 irghrkmvlytlrapr 102
                                                                                         27 hplgspgsasdletsglqeqrnhlqgklselqveqtsleplqesprptgvwksrevateg
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                                                                  1 HPLGSPGSASDLETSGLQEQRNHLQGKLSELQVEQTSLEPLQESPRPTGVWKSREVATEG 60
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IRGHRKMVLYTLRAPR 76
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1155 Avenue of the Americas
                                                                                                                                              56.8%; Score 392; DB 1; ilarity 100.0%; Pred. No. 1.3e-37. Conservative 0; Mismatches 0.
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99.3%;
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Pred. No. 1.4e-69;
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                                                                                                                                                                                 Length 76
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RESULT 5
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 71; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 11-JWN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, Kate H
NAME: MUTAShige, Kate H
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LEWICKI, J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
APPLICANT: SCARBOROUGH, R.M.
APPLICANT: SCARBOROUGH, R.M.
APPLICANT: SCARBOROUGH, R.M.
APPLICANT: DEWICKING FOR THE STATE OF THE SCAR APPLICANT OF BRAIN NATRIUETIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SEILHAMER, J.J.
                                                                           118 GSLSGLGCNVLRRY 131
                                                                                                             121 ssssglgckvlrrh 134
                                                                                                                                                       58
                                                                                                                                                                           61 qtsleplqesprptgvwksrevategirghrkmvlytlraprspkmvqgsgcfgrkmdri 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 219,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 05-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2000 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                   HIDLEPLRQDRGLTEAWEAREAAPTGVLGPRSSIFQVLRGIRSPKTMRDSGCFGRRLDRI 117
                                                                                                                                                                                                                             MGPRMALPR-VLLLLFLHLLLLGCRSHPLGGAGLASEL--PGIQELLDRLRDRVSELQAE 57
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                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                      48.5%; Score 334.5; DB 53.0%; Pred. No. 8.9e-31 ative 20; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                          DB 2;
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RESULT 6 US-08-850-910A-46

Sequence 46, Application US/08850910A

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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-850-910A-41
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Patent, No. 5948761
GENERAL INFORMATION:
APPLICANT: SEILHAMER, J.J.
APPLICANT: SEILHAMER, J.J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE
                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/477
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200
PILING DATE: 31-MAY-1988
APPLICATION NUMBER: 07/200
FILING DATE: 31-MAY-1988
APPLICATION NUMBER: 07/200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/850,910A FILING DATE: 05-MAY-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: 07/477,226 APPLICATION NUMBER: 07/477,226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
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118 GSLSGLGCNVLRRY 131
                  121 ssssglgckvlrrh 134
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                                                                   58 RTDLEPLRQDRGLTEAWEAREAAPTGVLGPRSSIFQVLRGIRSPKTMRDSGCFGRRLDRI 117
                                                                                                                                                                                                      / Match 48.5%;
Local Similarity 53.0%;
les 71; Conservative 2
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORRISON & FUERSIER, LLE.
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
                                                                                                                                   TELEFAX:
                                                                                     1, Application US/08850910A 5948761
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internal
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Pred. No. 8.9e-31;
20; Mismatches 40;
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                Sequence 47, Application US/08850910A Patent No. 5948761
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Best Local
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
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FILING DATE: OF US/na/~~
CLASCT—
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MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, Kate H
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE
TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/477, 226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
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                                                                                                                         118 GSLSGLGCNVLRRY 131
                                                                                                                                          121 ssssglgckvlrrh 134
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1 MGPRWALPR-VLLLLFLHLLLLGCRSHPLGGAGLASEL--PGIQELLDRLRDRVSELQAE 57
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                  qtsleplqesprptgvwksrevategirghrkmvlytlraprspkmvqgsgcfgrkmdri 120
                                                                                                                                                                                              RTDLEPLRQDRGLTEAWEAREAAPTGVLGPRSSIFQVLRGIRSPKTMRDSGCFGRRLDRI 117
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                                                                                                                                                                                                                                                                                                                                        71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                      48.5%; Score 334.5; DB 2; 53.0%; Pred. No. 8.9e-31; ative 20; Mismatches 40;
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RESULT 8 US-08-850-910A-43

Sequence 43, Application US/08850910A Patent No. 5948761

GENERAL INFORMATION:

APPLICANT:

SEILHAMER, J.J. LEWICKI, J.

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Best Local Similarity
Matches 68; Conserv
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
FILING DATE: 07/299,880
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/850,910A FILING DATE: 05-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PINUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/295
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200
FILING DATE: 31-MAY-1988
119 GSLSGLGCNVLRKY 132
                            121 ssssglgckvlrrh 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                 59
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                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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ZIP: 20006-1888
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                                                                                                                                             LENGTH:
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                                                                                                                            MEPCAALPRALLLLLFLHLSPLGGRPHPLGGRSPAS--EASEASELLGRLKDAVSELQAE 58
                                                             QLALEPLRHRSHSPAAWPARGGTPRGVLAPHDSVLQALRRLRSPKMMHKSGCFGRRLDRI 118
                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                    202-822-0168
                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORRISON & FOERSTER, LLP
                                                                                                                                                                                                                                                                                                                    single
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                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                       Score 307; DB 2;
Pred. No. 1.2e-27;
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US-08-850-910A-30
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; FRAGMENT TYPE:
US-08-850-910A-43
 Sequence 30, Application US/08850910A Patent No. 5948761
GENERAL INFORMATION:
APPLICANT: SEILHAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
                                                                                                                                                                                                                                                                                                                                                     Matches
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FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: MUIAShige, Kate H
                                                                                                                                                                                                                                                                                                                                                                    uery Match
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TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A FILING DATE: 05-MAY-1997
CLASSIETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                            116 RIGSLSGLGCNVLRKY 131
                                                                                                                                                                                          119
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                                                                                                                                                                                                                                                         61
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OPERATING SYSTEM:
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CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Murashige, Karregistration NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                           rissssglgckvlrrh 134
                                                                                                                                                                                                                                          QLALEPLHRSHSPA---EAPEAGGTPRGVLAPHDSVLQALRRLRSPKMMHKSGCFGRRLD 115
                                                                                                                                                                                                                                                                                      MEPCAALPRALLLLLFIHLSPLGGRPHPLGGRSPAS--EASEASELLGRLKDAVSELQAE 58
                                                                                                                                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 131 amino acids
amino acid
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VENTION: RECOMBINANT TECHNIQUES FOR
VENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE
LEWICKI, J.
SCARBOROUGH, R.M.
                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                  42.0%; Score 289.5;
50.7%; Pred. No. 1.10
tive 13; Mismatches
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GENERAL INFORMATION:
APPLICANT: TANAKA, SHOJI
APPLICANT: MIMAMITAKE, YOSE
APPLICANT: KITAJIMA, YASUO

YOSHIHARU

1, Application US/07828450 5434133

APPLICANT: FURUYA, MAYUMI
APPLICANT: MATSUO, HISAYUKI
TITLE OF INVENTION: CUP ANALOG PEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:

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RESULT 10
US-07-828-450-41
; Sequence 41, Ap
; Patent No. 5434
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: 07/477
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299
FILING DATE: 19-JAN-1988
APPLICATION NUMBER: 07/206
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/206
FILING DATE: 31-MAY-1988
APPLICATION NUMBER: 07/206
FILING DATE: 31-MAY-1988
APPLICATION NUMBER: 07/206
FILING DATE: 31-MAY-1988
APPLICATION NUMBER: 07/206
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 202-887-1500
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MEDIUM TYPE: Diskette
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                                                                                                                       92 kmvlytlraprspkmvqgsgcfgrkmdrissssglgckvlrrh 134

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64 SSIFQVLRGIRSPKTMRDSGCFGRRLDRIGSLSGLGCNVLRRY 106
                                                                                                                                                                                                                                               32 pgsasdletsglqeqrnhlqgklselqveqtsleplqesprptgvwksrevategirghr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 2000 Peni
CITY: Washington
                                                                                                                                                                                                            16 PGAAGPPARQGLRAAG-------DGTDLEPLRQDRGLTEAWEAREAAPTGVLGPR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino ac
STRANDEDNESS:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-822-0168
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                                                                                                                                                                                                                                                                                                 43;
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                                                                                                                                                                                                                                                                                               Conservative
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14-JUN-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                                                                                                                                           29.3%; Score 202; DB 2;
41.7%; Pred. No. 6.9e-16;
1tive 14; Mismatches 34
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RESULT 11
US-08-297-330-2
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US-07-828-450-41
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Best Local Similarity
Matches 32; Conserv
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TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/025,935
FILING DATE: 03-MAR-1993
                                                                                                                                                     ZIF: 55402-4131

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM:
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Burnett, John C.
TITLE OF INVENTION: VASONAT
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-00S
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9437/94133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wei, Chi-Ming APPLICANT: Burnett, John
                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                   STREET: 3100 No. CITY: Minneapolis
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FILING DATE: 19920131
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1625 L STREET, N.W. CITY: WASHINGTON
                                                                                                                    FILING DATE:
                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                            COUNTRY:
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Woessner, Warren D.
                                                                                                                                                                                                                                                                                                                     X
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3100 No. 5583108west Center
                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.5%; Score 169; DB 1; llarity 100.0%; Pred. No. 7.6e-13; Conservative 0; Mismatches 0;
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Thereof
                                                                                                                                       US/08/297,330
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US-08-451-240-22
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US-08-297-330-2
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Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/08451240 Patent No. 5665704
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb fl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/451,240
FILING DATE:
                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362552
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
ANAMY: TURNING TOFFER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
TELEX: 910/371-7168

NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                 TELEPHONE: 415/225-8228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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                  TELEFAX:
                                                                                     REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0844P1C1
                                                                                                      NAME: Kubinec, Jeffrey S. REGISTRATION NUMBER: 36,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: of TO NO
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                                    415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mature human brain natriuretic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.5%; Score 169; DB 1; 100.0%; Pred. No. 7.6e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert S
                                                                                                                                                                                                                                                                                                   US/08/451,240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30,440
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; TYPE: amino acid ; TOPOLOGY: linear US-08-451-240-22

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δõ
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US-08-470-846A-3
                                       Query Match
Best Local Similarity
Matches 32; Conserv
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Best Local Similarity 100.
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,84
FILING DATE: 06-Jun-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION US/08/470,84
FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Oare, Davi
APPLICANT: McDowell,
APPLICANT: Burnier, J
TITLE OF INVENTION: R
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                     NAME: Rubinec, Jeffrey S.
REGIZFATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/3 FILING DATE: 06-JAN-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
103 spkmvqgsgcfgrkmdrissssglgckvlrrh 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 spkmvqgsgcfgrkmdrissssglgckvlrrh 134
                                                                                                                                                         LENGTH: 32 amino TYPE: Amino Acid TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SPKMVQGSGCFGRKMDRISSSSGLGCKVLRRH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08470846A
                                                                                                                                                                                           32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burnier, John

WENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
SEQUENCES: 43
                                       24.5%; Score 169; DB 2; ilarity 100.0%; Pred. No. 7.6e-13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McDowell, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oare, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cunningham, Brian C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lowe, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.5%; Score 169; DB 1; 100.0%; Pred. No. 7.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08/362552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/470,846A
                                                                                                                                                                                                                                                                                                                                             36,575
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                                                                           Length 32;
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                                       Gaps
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PCT-US94-12591-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: 612-33 IN 10: 2
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1-ENGTH: 32 amino acids
                                                                                                                                                                                                                            Sequence 22, Application PC/TUS9412591 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.5%; Score 169; DB 4; Best Local Similarity 100.0%; Pred. No. 7.6e-1 Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 03-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: WOESSNET, Warren D.
REGISTRATION NUMBER: 30,44
                                                                                                                                          APPLICANT: Genentech, Inc.
APPLICANT: Lowe, David
APPLICANT: Cunningham, Brian C.
APPLICANT: Oare, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-331
TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mayo Foundation for Medical Education and Research APPLICANT: 200 First Street S.W.
APPLICANT: Rochester, Minnesota 55905 USA
TITLE OF INVENTION: Vasonatrin Peptide and Analogs Thereof
NUMBER OF SEQUENCES: 17
                                                            APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: PEPTIDES
                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             103 spkmvqgsgcfgrkmdrissssglgckvlrrh 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3500 IDS (CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                       1 SPKMVQGSGCFGRKMDRISSSSGLGCKVLRRH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SPKMVQGSGCFGRKMDRISSSSGLGCKVLRRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application PC/TUS9402391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Schwegman, Lundberg & Woessner 3500 IDS Center
                                                                                                                      McDowell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
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                                                                                                                         Robert S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 32;
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patin (Geneatech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12591
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/15294
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 32.637
REGISTRATION NUMBER: 32.637
REGISTRATION NUMBER: 344P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-1249
TELEFHONE: 415/25-1249
TELEFAX: 415/25-1249
TELEFORMATION FOR SED ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                            Query Match 24.5%; Score 169; DB 4; ]
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 32; Conservative 0; Mismatches 0;
Length 32;
                                                                              Indels
                                                                              0;
                                                                            Gaps
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Search completed: April 27, 2000, 18:34:45
Job time: 3059 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model April 27, 2000, 18:28:39; Search time 16.7 Seconds (without alignments) 556.334 Million cell updates/sec

Run on:

PEP1 690 1 mdpqtapsrall111f1hla.....rkmdrisssg1gckv1rrh 134 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

225878 seqs, 69334122 residues

Searched:

225878

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

sp\_mhc:\* sp\_organelle:\* sp\_phage:\* sp\_phant:\* sp\_rodent:\* sp\_virus:\* sp\_vertebrate:\* sp\_uclassified:\* SPTREMBL\_12:\*

1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: Sp\_mamman:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	046541 ovis aries	O55086 mus musculu	Q9ygjl salmo salar	Q29130 tupaia bela	046540 ovis aries	Q13766 homo sapien	P79799 micrurus co	Q9y2y4 homo sapien	O70373 mus musculu	082861 acetobacter	Q28644 oryctolagus	Q9wt02 human herpe	Q9z1p7 mus musculu	Q9wxf7 rhodococcus	018212 caenorhabdi	Q69468 human herpe	Q24029 drosophila	024027 drosophila	Q24031 drosophila	Q24028 drosophila
ΩI	046541	055086	Q9YGJ1	Q29130	046540	Q13766	P79799	Q9Y2Y4	070373	082861	Q28644	Q9WT02	Q921P7	Q9WXF7	018212	969468	924029	924027	Q24031	024028
DB	9	11	13	9	ø	4	13	4	11	7	9	12	11	~	Ŋ	12	Ŋ	'n	ഹ	Ŋ
Length	129	121	152	155	152	151	139	487	1677	1326	1984	780	791	418	557	629	1065	1072	1072	1074
Query Match	50.1	24.9	17.9	17.2	16.2	15.9	13.1	12.4	11.8	11.4	11.2	10.9	10.9	10.8	10.8	10.8	10.8	10.8	10.8	10.8
Score	345.5	171.5	123.5	118.5	112	110	90.5	85.5	81.5	78.5	77.5	75.5	75.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5
Result No.	1	7	m	4	Ŋ	٥	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20
	Query Score Match Length DB ID	Query Score Match Length DB ID 345.5 50.1 129 6 046541	Ouery Score Match Length DB ID 345.5 50.1 129 6 046541 171.5 24.9 121 11 055086	Query Score Match Length DB ID 345.5 50.1 129 6 046541 171.5 24.9 121 11 055086 123.5 17.9 152 13 09YGJ1	Query       Score Match Length DB ID       345.5 50.1 129 6 046541       171.5 24.9 121 11 055086       123.5 17.9 155 13 Q9YGJ1       118.5 17.2 155 6 Q29130	Query       Score Match Length DB ID       345.5       50.1       171.5       24.9       121       123.5       17.2       18.5       17.2       18.5       17.2       18.5       18.5       6.22       11.2       15.6       6.46540       0       0	Query       Score Match Length DB ID       345.5       50.1       171.5     24.9       123.5     17.9       118.5     17.2       155     6 029310       110     15.2       16     4 013766	Query       Score Match Length DB ID       345.5 50.1 129 6 046541       171.5 24.9 121 11 055086       123.5 17.9 152 13 097GJ1       118.5 17.2 155 6 029130       118.5 17.2 155 6 046540       110 15.9 151 4 013766       90.5 13.1 39 13 797999	Query       Score Match Length DB ID       345.5 50.1 129 6 046541       171.5 24.9 121 11 055086       123.5 17.9 152 13 09YGJ1       118.5 17.2 155 6 022130       110 15.9 151 4 013766       90.5 13.1 139 13 P79799       96.5 12.4 487 4 09YZY4	Query       Score Match Length DB ID       345.5     50.1       171.5     24.9       123.5     17.9       118.5     17.2       118.5     17.2       110     15.9       10     15.9       10     15.9       10     15.9       10     15.9       10     15.9       10     17.6       10     17.6       10     17.9       10     17.9       11     17.4       12     14       4     4       11     17.4       11     17.4       12     4       4     4       12     4       4     4       13     4       12     4       13     4       14     17.6       15     16       17     17       18     167       11     070373	Score Match Length DB ID  345.5 50.1 129 6 046541  127.5 24.9 121 11 055086 123.5 17.9 152 13 095031 118.5 17.2 155 6 029130 110 15.9 151 6 046540 110 15.9 151 4 019766 90.5 13.1 139 13 P79799 85.5 12.4 487 4 097274 81.5 11.8 1677 11 070373 78.5 11.4 1326 2 082861	Query       Score Match Length DB     ID       345.5     50.1       123.5     12.1       123.5     17.9       123.5     17.9       123.5     17.9       123.5     17.9       124.9     152       12     15       12     15       12     15       12     15       13     13       14     1376       90.5     13.1       11     15.9       12     487       4     487       81.5     11.2       11.2     16.2       139     199       11     409       11     400       11     400       11     400       11     400       11     400       11     400       11     400       12     6       12     6       13     10       13     10       14     40       15     6       16     6       17     198       18     10       18     10       18     10       18     10	Query       Score Match Length DB     ID       345.5     50.1       171.5     24.9       123.5     17.9       123.5     17.9       123.5     17.9       124.9     121       125.1     090001       110.5     152.6       00.5     13.1       13.1     15.9       15.9     13.4       15.9     13.4       15.9     13.4       15.9     13.4       15.9     10.9       15.0     10.9       15.0     10.9       15.0     10.9       15.0     12.4       15.0     13.4       15.0     13.4       15.0     13.4       15.0     13.4       15.0     13.4       15.0     12.4       15.0     12.4       15.0     12.4       15.0     12.4       15.0     12.4       15.0     12.4       15.0     12.4       15.0     13.4       15.0     13.4       15.0     13.4       15.0     13.4       15.0     13.4       15.0     13.4       15.0     13.4 </td <td>Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.9 152 13 097GJ1 112 16.2 152 6 046540 110 15.9 151 6 046540 110 15.9 151 4 01766 90.5 13.1 139 13 P79799 85.5 12.4 487 4 097274 81.5 11.8 1326 2 082864 77.5 11.2 1984 6 028644 77.5 10.9 791 11 0931702</td> <td>Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.2 152 13 0976371 118.5 17.2 155 6 029330 112 16.2 152 6 046540 110 15.9 15.1 4 037766 90.5 13.1 487 4 097274 81.5 11.8 1677 11 070373 77.5 11.2 1984 6 028644 77.5 10.9 780 12 09WT02 75.5 10.9 780 12 09WT02 74.5 10.8 418 2 09WXP7</td> <td>Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 1123.5 17.2 152 6 026341 118.5 17.2 155 6 022130 110 15.9 151 4 013766 90.5 12.4 487 4 097274 81.5 11.4 132 6 046540 77.5 11.2 16.7 11 070373 75.5 10.9 780 12 09WT02 75.5 10.9 780 12 09WT02 75.5 10.9 781 11 098477 74.5 10.8 557 5 018212</td> <td>Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.9 121 11 055086 112 16.2 15.5 6 046540 110 16.2 15.2 6 046540 110 16.2 15.2 6 046540 110 15.9 131 13 P79799 85.5 12.4 487 4 097274 81.5 11.4 1326 2 08264 77.5 11.2 1984 6 028644 77.5 10.9 791 11 092177 74.5 10.8 418 2 098777 74.5 10.8 659 12 066468</td> <td>Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.2 152 6 046540 112 16.2 152 6 029330 112 16.2 152 6 046540 110 15.9 151 4 013766 90.5 12.4 487 4 097274 85.5 12.4 487 4 097274 85.5 11.2 1984 6 028641 77.5 11.2 1984 6 028644 77.5 10.9 780 12 0997702 74.5 10.8 557 5 018312 74.5 10.8 657 5 018312 74.5 10.8 1065 5 024029</td> <td>Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.2 152 13 0976J1 118.5 17.2 152 6 026540 110 15.9 151 4 013766 90.5 12.4 487 4 0972Y4 81.5 11.4 139 1 979799 85.5 12.4 487 4 0972Y4 81.5 11.4 136 2 082861 77.5 10.9 791 11 070373 75.5 10.9 791 11 0971P7 74.5 10.8 557 5 018212 74.5 10.8 1065 5 024029 74.5 10.8 1065 5 5 024029</td> <td>Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.2 152 1 097GJ1 118.5 17.2 155 6 046540 110 15.9 151 4 01766 90.5 13.1 139 13 P79799 85.5 12.4 487 4 097274 81.5 11.8 1326 2 082864 77.5 11.2 1984 6 028864 77.5 10.9 791 11 0921P7 74.5 10.8 418 2 0987E7 74.5 10.8 659 12 065468 74.5 10.8 659 12 065468 74.5 10.8 1065 5 024029 74.5 10.8 1065 5 024029</td>	Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.9 152 13 097GJ1 112 16.2 152 6 046540 110 15.9 151 6 046540 110 15.9 151 4 01766 90.5 13.1 139 13 P79799 85.5 12.4 487 4 097274 81.5 11.8 1326 2 082864 77.5 11.2 1984 6 028644 77.5 10.9 791 11 0931702	Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.2 152 13 0976371 118.5 17.2 155 6 029330 112 16.2 152 6 046540 110 15.9 15.1 4 037766 90.5 13.1 487 4 097274 81.5 11.8 1677 11 070373 77.5 11.2 1984 6 028644 77.5 10.9 780 12 09WT02 75.5 10.9 780 12 09WT02 74.5 10.8 418 2 09WXP7	Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 1123.5 17.2 152 6 026341 118.5 17.2 155 6 022130 110 15.9 151 4 013766 90.5 12.4 487 4 097274 81.5 11.4 132 6 046540 77.5 11.2 16.7 11 070373 75.5 10.9 780 12 09WT02 75.5 10.9 780 12 09WT02 75.5 10.9 781 11 098477 74.5 10.8 557 5 018212	Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.9 121 11 055086 112 16.2 15.5 6 046540 110 16.2 15.2 6 046540 110 16.2 15.2 6 046540 110 15.9 131 13 P79799 85.5 12.4 487 4 097274 81.5 11.4 1326 2 08264 77.5 11.2 1984 6 028644 77.5 10.9 791 11 092177 74.5 10.8 418 2 098777 74.5 10.8 659 12 066468	Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.2 152 6 046540 112 16.2 152 6 029330 112 16.2 152 6 046540 110 15.9 151 4 013766 90.5 12.4 487 4 097274 85.5 12.4 487 4 097274 85.5 11.2 1984 6 028641 77.5 11.2 1984 6 028644 77.5 10.9 780 12 0997702 74.5 10.8 557 5 018312 74.5 10.8 657 5 018312 74.5 10.8 1065 5 024029	Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.2 152 13 0976J1 118.5 17.2 152 6 026540 110 15.9 151 4 013766 90.5 12.4 487 4 0972Y4 81.5 11.4 139 1 979799 85.5 12.4 487 4 0972Y4 81.5 11.4 136 2 082861 77.5 10.9 791 11 070373 75.5 10.9 791 11 0971P7 74.5 10.8 557 5 018212 74.5 10.8 1065 5 024029 74.5 10.8 1065 5 5 024029	Score Match Length DB ID  345.5 50.1 129 6 046541  171.5 24.9 121 11 055086 123.5 17.2 152 1 097GJ1 118.5 17.2 155 6 046540 110 15.9 151 4 01766 90.5 13.1 139 13 P79799 85.5 12.4 487 4 097274 81.5 11.8 1326 2 082864 77.5 11.2 1984 6 028864 77.5 10.9 791 11 0921P7 74.5 10.8 418 2 0987E7 74.5 10.8 659 12 065468 74.5 10.8 659 12 065468 74.5 10.8 1065 5 024029 74.5 10.8 1065 5 024029

Q24030 drosophila Q79795 human immun Q96698 drosophila Q80113 homo sapien Q60392 homo sapien Q60392 human immun Q65240 arabidopsis Q96554 cryptcospori Q21879 bacterlopha Q62308 mus musculu Q97556 homo sapien Q00819 cryptcococcu Q922K7 mus musculu Q97632 homo sapien Q15858 homo sapien Q15858 homo sapien Q22860 caenorhabdi Q52316 klebsiella Q05318 homo sapien Q22861 demo sapien Q23861 demo sapien Q92381 mus musculu Q94618 mus musculu Q94618 mus musculu Q95996 homo sapien Q92861 demo sapien Q92861 demo sapien Q92861 demo sapien Q924861 musculu Q94618 mus musculu	mus mus mous
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                        OGAWA Y., ITOH H., TAMURA N., SUGA S., YOSHIMASA T., UEHIRA M.,
MATSUDA S., SHIONO S., NISHIMOTO H., NAKAO K.;
"Molecular cloning of the complementary DNA and gene that encode mouse
brain natriuretic peptide and generation of transgenic mice that
overexpress the brain natriuretic peptide gene.";
J. Clin. Invest. 93:1911-1921(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Two cardiac natriuretic peptide genes (atrial natriuretic peptide and brain natriuretic peptide) are organized in tandem in the mouse and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 gtsleplgesprptgvwksreva----tegi-rghrkmvl----ytlra---prspkm 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 mdpqtapsralllllllhlaflggrshplgspgsasdletsglqeqrnhlqgklselqve 60
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostei; Euteleostei; Protacanthopterygil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.9%; Score 171.5; DB 11; Length 121; 36.3%; Pred. No. 4.2e-10; Live 19; Mismatches 33; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TERVONEN V., ARJANAA O., RUSKOAHO H., VUOLITEENAHO O.;
"New vascactive cardiac hormone released by mechanical load.";
submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                            Mammalia;
Mus.
                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CARDIAC HORMONE (CARDIAC PEPTIDE PRECURSOR).
                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0710; NATPEPTIDES.
PRINTS; PR00712; BNATPEPTIDE.
SEQUENCE 121 AA; 13730 MW; E3BFECOB CRC32;
                       121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human genomes.";
J. Wol. Cell. Cardiol. 28:1811-1815(1996).
EMBL; D82049; BAA24159.1; -.
PROSITE: PS00263; NATRIORETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMURA N., OGAWA Y., YASODA A., NAKAO K.;
                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 vggsgcfgrkmdrissssglgckvlr 132
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                         PRT;
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                                                                     01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 36.3%
Matches 53; Conservative
                                                                                                                                                   BRAIN NATRIURETIC PEPTIDE.
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                         PRELIMINARY;
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MEDLINE; 94237953.
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MEDLINE; 97031884.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Q9YGJ1;
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09YGJ1
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70 DEAGAALSPLPEVPPWTGEVSPAQRDGGALGRSPWDSSE-----RSALLKSKLRAM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 qtapsralllllflhlaflggrshplgspgsasdletsglqeqrnhlggklselqveqts 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---revate----girghrkmvlyt 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 5-152 FROM N.A.
MAJALAHTI-PALVIAINEN T., HIRVINEN M., TERVONEN V., VUOLTEENAHO O.;
"Gene structure of a novel cardiac peptide related to natriuretic
peptides from Salmo salar.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ001806; CAA05022.1;
EMBL; AJ006421; CAA07023.1; -.
PROSIȚE; PS00263; NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 17.9%; Score 123.5; DB 13; Length 152; Best Local Similarity 32.1%; Pred. No. 3.5e-05; Matches 50; Conservative 14; Mismatches 55; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Scandentia; Tupalidae; Tupala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases EMBL; 270294; CAA94310.1; -. PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCHNEIDEMANN S., MAEGERT H.J., FORSSMANN W.G.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last annotation update) CARDIODILATIN, ATRIAL NATRIURETIC PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.2%; Score 118.5; DB 6; 29.7%; Pred. No. 0.00011; tive 15; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 lllflhlaflggrshplgsp--gsasdletsglgegrnhlggkl
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PRINTS; PR00711; ANATPEPTIDES.
PRINTS; PR00711; ANATPEPTIDE.
SEQUENCE 155 AA; 16860 WW; 77E8CA8B CRC32;
                                                                                                                                                                                                                                                                    124 152 CARDIAC HORMONE.
152 AA; 16740 MW; 1B46F303 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 lraprspkmvqgsgcfgrkmdrissssglgckvlrr 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 lraprspkmvqgsgcfgrkmdrissssglgckvlr 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 29.7%
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARDIGOL A.;
                                                                                                                                                                                                                                            Signal.
CHAIN
SEQUENCE
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Q29130;
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Gaps

48;

Length 151; Indels -----1selqve 60

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RESULT 104 6 540 104 6 540 104 6 540 105

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HO P.L., SOARES M.B., MAACK T., GIMENEZ I., PUORTO G., FURTADO M.F.D., RAW I.;
"Cloning of an unusual natriuretic peptide from the South American coral snake Micrurus corallinus.";
Eur. J. Blochem. 250:144-149(1997).

EMBL: U77596; AAC60341.1;
EMBL: U77596; AAC60341.1;
PROSITE; PSO0263: NATRURETIC_PEPTIDE; 1.
PFAM: PFO0212; ANP: 1
PRINTS; PRO0710; NATPEPTIDES.
SEQUENCE 139 AA; 14881 MW; 05421ABB CRG32;
                                                                                                                                                                                                                                                                                                                                                                                           70 AGAALSPLPEVPPWTGEVSPAQRDGGALGRGPWDSSD------RSALLKSKLRALLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtsleplqesprptgvwksrevategirghrkmvlytlraprspkmvggsgcfgrkmdri 120
                                                                                                                                                                                                                                                   12 LILLAFQLLGQTRANPMYNAVSNADL--MDFKNLLDHLEEKMPLEDEVVPPQVLSDPNEE 69
                                                                                                                                                                                                                                                                                                                                  61 q-tsleplqesprpt-----lr 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapinae;
                                                                                                                                                                                                             14 llflhlaflg-grshplgspgsasdletsglgegrnhlggk-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
NATRIURETIC PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Pred. No. 0.064;
9; Mismatches 25;
                                                                                     Query Match 15.9%; Score 110; DB 4; Best Local Similarity 30.1%; Pred. No. 0.00078; Matches 46; Conservative 17; Mismatches 42
151 AA; 16381 MW; E8827DA3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 aprspkmvggsgcfgrkmdrissssglgckvlr 132
|||| :: | ||| :|||| |
|121 aprs---LrrsScrgGrmdrigaQsGLGCNSFR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-VENOM GLAND;
HO P.L., SOARES M.B., YAMANE T., RAW I.;
J. TOXICOl. TOXIN. Rev. 14:327-337(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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Best Local Similarity 31.9%;
Matches 23; Conservative 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNVSGMGCNHVR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Micrurus corallinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-VENOM GLAND;
MEDLINE; 98092299.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Micrurus
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P79799;
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Q9Y2Y4;
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P79799
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DT 01
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ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 SEQNEEAGAPLSPLSEVPPWDGGRST --- OPREMGAPSDGDPGNPPRSVLLKSKLRALLT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 sralllllflhlaf-lggrshplgspgsasdletsglgegrnhlggkl-----selg 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 veqts----leplqesp----rptgvwksreva--tegirgh--rkmvlyt----lr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
ALTENS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.;
ALTEN G.D., RAIZIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.;
SUBMILTED (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF037465; AAB92564.1; -.
PROSTIE; PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
PFAM; PF00212; ANP; 1.
PFRM; PR00710; NATPETIDES.
SEQUENCE 152 AA; 16368 MW; D5360BCC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X SEQUENCE FROM N.A.

MEDLINE; 85206210.

A SEIDMAN C.E., BLOCH K.D., ZISFEIN J., SMIT J., HABER E., HOMCY C., BLOWY A.D., CHOI E., GRAHAM R.M., SEIDMAN J.G.;

I "Molecular studies of the atrial natriuretic factor gene.";

Hypertension 7:31-34(1985).

R EMBL; M45947; AAA35529.1; -.

R EMBL; M54951; AAA35529.1; -.

R PRIMT; PS00212; ANP: 1.

R PRIMTS; PR00710; NATRIURETIC_PEPTIDE; 1.

R PRIMTS; PR00711; ANATPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                              Ovis aries (Sheep).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.2%; Score 112; DB 6; Length 152; 30.7%; Pred. No. 0.0005; Live 24; Mismatches 48; Indels
                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ATRIAL NATRIURELIC FACTOR PRECURSOR.
121 LAAPRS---LRRSSCFGGRMDRIGAQSGLGCNSFR 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 aprspkmvqgsgcfgrkmdrissssglgckvlr 132
                                                                                                                                                                                                                Created)
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                                                                                                                                                    PRT;
                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-NOV-1999 (TrEMBLrel. 12, ATRIAL NATRIURETIC PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.7'
Matches 47; Conservative
                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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PEPTIDE
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013766;
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Indels 15; Gaps

101376 101376

RESULT

셤 ò g ö 셤 Length 139;

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61 gts-----leplgesprptgvwksrevategirghrkmvlytlraprspkmvggs 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 dpg-tapsrallllflhlaflggrshplgspgsasdletsglgegrnhlggklselgve 60
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SYRIN-WAN ZEALAND WHITE; TISSUE-SCIATIC NERVE;
MEDLINE; 96074641.
BELCHER S.M., ZERILLO C.A., LEVENSON R., RITCHIE J.M., HOWE J.R.;
"Cloning of a sodium channel alpha subunit from rabbit Schwann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAKAI T., MORIYA A., TONOUCHI N., TSUCHIDA T., YOSHINAGA F., HORINOUCHI S., SONE Y., MORI H., SAKAI F., HAYASHI T.; "Control of expression by the cellulose synthase (bcsA) promoter region from Acetobacter xylinum BPR 2001."; Gene 213:93-100(1999).
                                                                                                                                                                                                                                                                                  Acetobacter xylinum (Acetobacter pasteurianus).
Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.\,; to the EMBL/GenBank/DDBJ databases
                                                                                             (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB010645; BAA31465.1; -.
SEQUENCE 1326 AA; 142103 MW; F49C1753 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                    PRT; 1326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1984 AA
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24.0%; Pred. No. 12;
tive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                          CELLULOSE SYNTHASE SUBUNIT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999 (TrEMBLrel. 12, SODIUM CHANNEL ALPHA-SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 24.0
Matches 29; Conservative
                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMEYAMA T., TONOUCHI
Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BPR2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BPR2001;
MEDLINE; 98296257.
                                                                                                                                                                                                                                                                                                                                                       Acetobacter.
                                                                082861;
01-NOV-1998
                                                                                                                                                                      01-NOV-1998
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082861
ID 082861
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Q28644
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                                       SORETERANCOS REPRESENTANTOS SORETERAN SORTERAN SO
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WANG D.-Z., HU X., LIN J.L.-C., KITTEN G.T., SOLURSH M., LIN J.J.-C.;
Front. Biosci. 1:0-0(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 gv-----wksr----evategirghrkmvlytlraprspkmvqgsgcfgrkmdrisss 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 GVOSLEEACWRARGDRAKKPDPGLKKHQE---EPEKPSRNPERELGDPGEKQKPEQVSRT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 RGRLPGNLCQVATSRPPLESLRKAPLPTAQIRSRRTSRSGGDVQAARQMFETKPLDALRG 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 hlaflggrshplgspgs---asdletsglqeqrnhlqgklselqveqtsleplqesprpt 74
                                                                                                                                                                                                      TISSUE-TESTIS;
TANG T.*, LAI C.-H., TANG C.-J., HUANG C.-J., LIN W.-C.;
Identification and gene structure of a novel human PLZF related
transcription factor gene, TZFP.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF130255 AAD27708 11;
SEQUENCE 487 AA; 52962 MW; E3F0D6BF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
Mus.
                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 12.4%; Score 85.5; DB 4; Length 487; Local Similarity 25.2%; Pred. No. 0.81; les 33; Conservative 24; Mismatches 55; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF051945; AAC06023.1; -.
MGD; MGI:1333878; X110.
SEQUENCE 1677 AA; 182085 MW; 106A30FA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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25.8%; Pred. No. 8;
tive 15; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 rnhlqgklselqveqtsleplqesprptgvwksrevateg---
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   TESTIS ZINC FINGER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Conservative
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TISSUE=CARDIAC MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 GGREQEMLHKH 168
                                                                                                                                                                             SEQUENCE FROM N.A.
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EF89D962 CRC32; 1984 AA; 225748 MW; Ionic channel SEQUENCE 19

RESULT 10

Matches

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34;
                                   Query Match
Best Local S
Matches 34
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SUNAGAWA T., SASHHARA J., ZOU P., KOSIGE H., YAMANISHI K.;
SUNAGAWA T., SASHHARA J., ZOU P., KOSIGE H., YAMANISHI K.;
6 variant A and B.";
J. Virol. 0:0-0(1999)
EMBL; AB021506: BAA78294.1;
SEQUENCE 780 AA; 89540 MW; 5F3A240A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 GRSRIMGLSESSSETSKLSSKSAKERRNRRKKKNOKKLSSGE-EKGDDEKLSKSESEESI 507
                                                                                                grshplg---spgsasdletsglgegrnhl----ggklselgvegtsleplgesprptgv 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROWEN L., QIN S., MADAN A., LORETZ C., HALL J., JAMES R., DORS M., SHAFFER T., ABBASI N., RATCLIFFE A., DICKHOFF R., LASKY S., HOOD L.; "Sequence of the mouse major histocompatibility complex class II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 llllflhlaf--lggrshplgspgsasdletsglqeqrnhlggklselqveqtsleplqe 69
                                                            11;
                 Length 1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 780;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                     77 wksrevategirghrkmvlytlrap-rspkmvggsgcfgrkmdrissssglg 127
                                                                                                                                                                                                           --SRKQFHLGVEGHRLAREKRLSAPNQSPLSIRGSLFSARRSSRTSLFSFKG
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; #47110520; AAC97966.1; -.
HSSP; P42773; 1BU9.
SEQUENCE 791 AA; 84186 MW; 495A3736 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 sprptgvwksrevategirghrkmvlytlraprspkmvqgsgcfgr 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 75.5; DB 12;
; Pred. No. 14;
13; Mismatches 47;
                 DB 6;
11.2%; Scc. 32.1%; Pred. No. 27, 32.1%; Pred. No. 27, 41; Mismatches
                                                                                                                                                                                                                                                                                                                                        780 AA.
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ilarity 27.4%;
Conservative 13
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN BINDING PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human herpesvirus 6.
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Best Local Similarity
Matches 29; Conserv
                                      Similarity
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SEQUENCE FROM N.A.
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01-NOV-1999
01-NOV-1999
                    Local Sun.
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                    Query Match
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Q921P7
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                                                          Matches
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                                                                                     Gaps
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TAKIZAWA N., FUJIWARA T., HATTA T., FUKUDA M., KIYOHARA H.;
"Cloning, nucleotide sequence, and characterization of naphthalene
degradation genes, rno, of gram-positive bacteria Rhodococcus sp.
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Rhabditina, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
    Length 791;
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EMBL; AB024936; BAA76335.1; -.
SEQUENCE 418 AA; 46506 MW; 12CB0554 CRC32;
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DB 11;
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A WILSON R., BURTON J., CONNELL M., COPSEY T., COOPER J., COLLSON A.,
A CRAXTON M., DERR S., DU Z., DURBLIN R., FAVELLO A., FULLON L.,
CRAXTON M., DERR S., DU Z., DURBLIN R., FAVELLO A., FULLON L.,
A GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L.,
A JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
A LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHRAN M.,
PARSONS J., PERCY C., RIFKER L., SOONFA A., SHOWNKEEN R.,
A THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGRAN K., WATERSTON J.,
A THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGRAN K., WATERSTON R.,
A HATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
I NATLING J., THOMAS R., SOONHAMMER E., STADEN R., MATERSTON R.,
A HERRY-MIEG J., THOMAS K., VAUDIN M., VAUGRAN K., WATERSTON R.,
A HERRY-MIEG J., THOMAS R., WILKINSON-SPROAT J., WOHLDMAN P.;
I NATLING JSS 32373; CAB164871; -.
IS REALL: 299277; CAB164871; -.
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. \{2\}
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; 0 Query Match 10.8%; Score 74.5; DB 5; Length 557; Best Local Similarity 21.2%; Pred. No. 12; Matches 32; Conservative 26; Mismatches 50; Indels 43; Gaps 11 lllllflhlaf---lggrshplgspgsasdletsglqeq------rnhlq--- 52 : |: | || || ||:: | 370 TPIVKLPCAVDIVKHPMEKNSKSSALHCKIV 400 103 --spkmvggsgcfgrkmdrissssglgckvl 131 g ò. ò 셤 ò

Search completed: April 27, 2000, 21:53:26 Job time: 12287 sec

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G09534 human STS C
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M3177 Dog brain n
E05300 DNA encodin
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E02602 692 bp RNA PAT 29-SEP-1997 DNA encoding human brain natriuretic peptide(human BNP). E02602 E02602. GI:2170830 JP 1990231082-A/1.

LOCUS DEFINITION ACCESSION VERSION KEYWORDS

RESULT

ALIGNMENTS

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/product='human brain natriuretic peptide' FT
/note='hBNP'
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                  Vertebrata; Mammalia; Eutheria;
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/note='pre precursor peptide'
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406. .501
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anti-sense: No;
*source: tissue_type=atrium;
*source: clone=lambda hBNP-57;
Location/Qualifiers
                                                   Sudo, T., Maekawa, K., Minamino, N., Sagawa,
NOVEL DNA FRAGMENT
                  Eukaryota; Metazoa; Chordata; Vertebra
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 692)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
197 c 196 g 14
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cloning and sequence analysis of cdna encoding a precursor for human brain natriuretic peptide
Biochem. Biophys. Res. Commun. 159, 1427-1434 (1989)
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                                                                                              27-APR-1993
                                                                                                                                                               natriuretic peptide.
Homo sapiens (library: lambda gt10) adult brain cDNA to mRNA.
                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 692)
Sudoh,T., Maekawa,K., Kojima,M., Minamino,N., Kangawa,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 TICCTGGGAGGTCGTTCCCACCGCTGGGCAGCCCCGGTTCAGCCTCGGACTTGGAAACG
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                                                                                                               complete cds
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                                                                                              HUMNATPEP 692 bp mRNA
Human natriuretic peptide precursor mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 402; DB 9;
Pred. No. 1.8e-91;
460 AGCTCCTCCAGTGGCCTGGGCTGCAAGTGCTGAGGCGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Scor.
100.0%; Pred. No. 1...
... 0; Mismatches
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Best Local Similarity 100.
Matches 402; Conservative
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
Primates; Catarrhini; Hominidae; Homo.
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human brain natriuretic peptide.
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Pred. No. 4.8e-71;
0; Mismatches 2;
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/db_xref="taxon:9606"
239 c 226 q 197
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Location/Qualifiers
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                                                       E04396 888 bp
DNA sequence encoding hu
E04396 E04396.1 GI:2172597
JP 1993056794 A/1.
Homo sapiens.
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Best Local Similarity 99.4%;
Matches 322; Conservative 0
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E04438
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RESULT 3
E04396
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Eukaryota: Metazoa; Chordata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eukaryota: Metazoa; Chordata; Homo.

1 (bases 1 to 888)

Mori, T., Maekawa, K., Izumi, A. and Sudo, T.

PRODUCTION OF PHYSIOLOGICALLY ACTIVE PEPTIDE

PRODUCTION OF PHYSIOLOGICALLY ACTIVE PEPTIDE

DAI ICHI PURE CHEM CO LTD, DAI ICHI SEIYAKU CO LTD

OS Homo sapiens (human)

PN 1919306881-A/1

PD 23-MAR-1993

PF 10-SEP-1991 JP 1991230597

PF 10-SEP-1991 JP 1991230597

PF 10-SEP-1991 JP 1991230597

PF 10-SEP-1991 JP 1991230597

C12P21/02,

C12P21/02,

C21P21/02,

C21P21/02,

C2 Strandedness: Double;

CC Anti-sense: No:

CC anti-sense: No:

CC Anti-sense: No:

CC *source: clonePKKmIhB;

FH Key

FT misc_feature 1: .888

FT misc_feature 1: .888

FT FT MISC_Feature 1: .888
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 239 c 226 g 19
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                 Homo sapiens.
Homo sapiens
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/map="p36.21"
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                                                                                                              SOURCE
            Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (Dases 1 to 1922)
Scilhamer, J. J., Arfsten, A.E., Miller, J. A., Lundquist, P.,
Scarborough, R.M., Lewicki, J.A. and Porter, J.G.
Human and canine gene homologs of porcine brain natriuretic peptide
Blochem. Blophys. Res. Commun. 165, 650-658 (1989)
                                                                                                                                                                                                                                                                                                                             /protein_id="AAA35603.1"
/db_xref="G1:179515"
/db_xref="G1:179515"
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/db_xref="G1:179515"
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FQRNHLQGGLSELQVEQTAPPROTEDFLOGSPRPTGWKSREVATEGIRGHRKMVLYTLRAPR
SPKMYGGSGCFGRKMDRISSSSGLGCKVLRRH"
<498. 629
/note="brain natriuretic protein"
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                               400. .1864

/note="brain natriuretic protein mRNA and introns"

/note="brain natriuretic protein"

/note="brain natriuretic protein"

/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             630. .860
/note="brain natriuretic protein, intron A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1117. .1658
Anote-"brain natriuretic protein, .1659. .21675
Anote-"brain natriuretic protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 260.4; DB 9;
Pred. No. 7.1e-56;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421
                                                                                                                                                                        1. .1922
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.88;
99.68;
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552 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261; Conservative
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                                                                                                                                                                                                                                     prim_transcript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430
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HS934G17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                            TITLE
JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
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(http://www.sanger.ac.uk/HGPC/hrl/) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquires: Connective the constant of clone 934617. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at hitp://www.sanger.ac.uk/HGP/Chil/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
                                                                                                                                       HTG; ANF; ANP; Atrial Natriuretic Factor; Atrial Natriuretic peptide; BNP; Brain Natriuretic Protein; chloride chanel; CLC-6; CLCN6; DIS2740; KIAA0046; Myotubularin-related protein; NPPA; SBF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: cDNA x99473 x83378 D28475; match: ESTS
H08286 N25443 H08188 R21038 H87122 T95239 T97238 AA412325
H08286 N25443 H08188 R210538 H87122 T95249 T97228 AA412325
T97200 F07103 AA806700 T97201 AA488792 AA046481 AA366116
T445501 AA321539 F03382 H83350 AA6025387 AA772135 N20380
R41299 R98117 AA855134 T28428 R16666 N36430 H87016 R96814
H81752 AA026032 AA613847 AA046694 AA489008"
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/note="AluSx repeat: matches 302. .1 of consensus"
/note="AluSx repeat: matches 302. .1 of consensus"
/loin(<1360. .1425,2129. .2194,5002. .5068,8209. .8315,
9221. .9347,10000. .10067,11670. .11728,12603. .12735,
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19391. .19544,19750. .19909,19998. .20104,21481. .21667,
22513. .22670,22857. .23013,23849. .23956,24049. .24174,
25657. .22648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The true left end of clone 934G17 is at 1 in this sequence. The true right end of clone 934G17 is at 107603.
934G17 is from the library RPCI5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/product="dJ34G17.1.1 (chloride chanel protein CLC-6A
(KIRA0046)) (isoform 1)"
1360. .2947
                                                                                                                                                                                                                                                                                                                                                                      Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note""AluY repeat: matches 1. .298 of consensus"
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STSs and the genomic marker DIS2740, complete sequence.
AL021155
AL021155.1 GI:3171888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Errington, H.
Direct Submission
Submitted (12-MAY-1998) Chromosome 1 Project Group
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107603)
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CDS

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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                VGAGLPOFOSISLRKIOFNFPYFRSDRYGKROERLCISRSGCWSCCSFRGANNGYLVV
SRGGFYLLEPRAHVESALLFHYCHLAPOLLEPWDSVWKLGFLPAPWIAELWRW"
Join (<1360. 10425, 2129. 2194, 5002. 5068, 8209. 8315,
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13620. 13733, 14710. 14817)
Agene "CLING"
/note-"match: protein Q99428; match: cDNA X99474"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVAAGSGIPPWCYLLKGVKVPGIVRLATLLCKVLGYLFSVAGGLFVEKEGPANHSGSV
VGAGLPQFQSISLRKIQFNFPYFRSDRSGCWSCCSFRGANRGYLVQSRGGFVLLEPRA
HVESALLFHVCHLHPQLLPFWDSVWKGFLPAPWIAELWRV
1011(<1360. 11425, 2129. 21294, 5002. 5068, 8209. 8315,
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13620. 13733, 13972. 14118, 14110. 14836, 19029. 19152,
19391. 119544, 19750. 19909, 19998. 20104, 21481. 21667,
22513. 22670, 22857. 23013, 23849. 23956, 24049. 24174,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGLEVDEFVRLFTQLKFGVVQTSVEECSQKGCLALSLLELLGFNLTFVFLASLLVLIE
PVAAGSGIPEVKCYLNGVKVPGIVRLRTLLCKVLGVLFSVAGGLFVEKEGPMIHSGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGAGLPQFQSISLRKIQFNFPYFRSDRDKRDFVSAGAAAGVAAAFGAPIGGTLFSLEE
GSSFWNQGLTWKVLFCSMSATFTLNFFRSGIQFGSWGSFQLPGLLNFGEFKSLREPPC
VSGNHRGGVCGLDGVRRMPTDVLFESHR"
join (<1360. 1425, 2129. 2194, 5002. 5068, 8209. 8315,
9221. 9347, 10000. 10067, 11670. 11728, 12629. 12735,
13620. 13732)
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/translation="ELDYDRCINDFYLEVLETMDNKKGRRYEAVKWWVFAIGVCTGL
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VGAGLPOFOSISLRKTOFNPFYFSDRDKRDFVSAGAAAGVAAAFGAPIGGTLFSLEE
GSSFWNQGLTWKVLFCSMSATFTLNFFRSGIQFGSWGSFQLPGLLNFGEFKCSDSDKK
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                                                                                                                                                                                                                                                 (isoform 2)
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CDS

VTTVVVFVASMVLGECRQMSSSSQIGNDSFOLQVTEDVNSSIKTFFCPNDTYNDMATL FFNPOESAILQLFHQDGTFSPVTLALFFVLYFLLACMTYGTSVPSGLEVPSILCGAAF GRLVANVLKSYIGLGHIYSGTFALIGHAAFLGGVVRMTISLTVILIESTNEITYGLPI MYTLMVAKMTGDFFRKGIYDIHVGLRGVPLLEWETEVEMDKLRASDIMEPNLTYVYPH TRIOSLVSILRTTVHHAFPVVTENRGNEKEFWKGNQLISNNIKFKKSSILTRAGEQRK RSQŠMKSYPSSELRNMCDEHIASEEPAEKEDLLQQMLERRYTPYPNLYPDQSPSEDWT MEERFRPLIFHGLILRSQLVTLLVRGVCYSESQSSASQPRLSYAEMAEDYPRYPDIHD LDLTLLNPRMIVDVTPYMNPSPFTVSPNTHVSQVFNLFRTMGLRHLPVVNAVGEIVGI ö CHLWTAMDLGFFVVMGVIGGLLGATFNCLNKRLAKYRMRNVHPKPKLVRVLESLLVSI 1547. .1665 /note="TrGGER1 repeat: matches 1. .127 of consensus" 1670. .1885 /note="TrGGER1 repeat: matches 2200. .2417 of consensus" 2600. .2751 /note="AluJo repeat: matches 302. .156 of consensus; on 3780. .4003.

// note-"MER46 repeat: matches 1. .133 of consensus"
// note-"MER46 repeat: matches 234. .1 of consensus"
// note-"FLAM\_A repeat: matches 1. .124 of consensus"
// note-"MER30 repeat: matches 172. .1 of consensus"
// note-"AluJo repeat: matches 158. .290 of consensus;
// note-"AluJo repeat: matches 158. .290 of consensus;
// note-"AluJo repeat" 43870 GCCACCGAGGCATCCGTGGGCACCGCAAAATGGTCCTCTACACCCTGCGGGCACCACGA 43810 43809 AGCCCCAAGATGGTGCAAGGGTCTGGCTTTTGGGAGGAAGATGGACCGGATCAGCTCC 43750 246 127 ttacaggagcagcaaccatttgcagggcaaactgtcggagctgcaggtggagcagaca 186 /note-"Alusx repeat: matches 1. .301 of consensus" 7089. .7204
/note-"Alus4 repeat: matches 22. .138 of consensus" 7774. .8056
/note-"AlusD repeat: matches 299. .1 of consensus" 8507. .8659. .105 consensus" /note-"Lipal6 repeat: matches 724. .904 of consensus" /note="MER5A repeat: matches 85. .171 of consensus" 10511. .10631 8723. .9011 /note="AluSp repeat: matches 35. .303 of consensus; 5999. . 6299 /note="AluY repeat: matches 1. .300 of consensus" 6307. .6608 /note="AluSq repeat: matches 1. .303 of consensus" 6790. .7088 tccctggagccctccaggagagccccgtcccacaggtgtctggaagtcccgggaggta 43929 TCCCTGGAGCCCCTCCAGGAGAGCCCCCGTCCCACAGGTGTCTGGAAGTCCCGGGGAGGTA gccaccgagggcatccgtgggcaccgcaaatggtcctctacaccctgcgggcaccacga agccccaagatggtgcaagggtctggctgttgggaggaagatggaccggatcagctcc 64.8%; Score 260.4; DB 11; Length 107603; 99.6%; Pred. No. 5.6e-56; ive 0; Mismatches 1; Indels 0; G incomplete repeat" 3494. :3628 /note="FLAM\_C repeat: matches 1. 3780. :4003 ITRHNLTYEFLQARLRQHYQTI" ncomplete repeat" 43749 TCCAGTGGCCTGGGCTGCAAAG 43728 tccagtggcctgggctgcaaag 388 Conservative

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5
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Maekawa, K., Sudo, T., Minamino, N., Sagawa, K., Okubo, H., Nakanishi, S.
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0.5EB-1990
22-FEB-1989 JP 1989042720
MAEKAWA KEIJI, SUDO TETSUJI, MINAMINO NAOTO, SAGAWA KENJI,
                                                                                                                                                                                                                                                                                                                                                                           lrain naturiuretic peptide
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        PAT 29-SEP-1997 hog brain natriuretic peptide.
                                                                                                                                                                                                                                                                                                                                                                                    otide 50. .124

Product-'signal peptide of hog lrain natriuretic peptide'
tide 125.442

/product-'mature peptide of hog lrain natriuretic peptide'
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C12N15/16,A61K37/02;
strandedness: Double;
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Pred. No. 9.1e-36;
0; Mismatches 114;
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                                                                                                                                                  Patent: JP 1990222683-A 1 05-SEP-1990;
DAI ICHI SEIYAKU CO LTD, DAI ICHI PURE
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50. .445
/product='hog
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/organism="unidentified"
/db_xref="taxon:32644"
1 200 c 193 g 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             443. .625
polyA_site 556. .561
misc_difference 76
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    CDNA sequence encoding
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hypothetical: No;
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Best Local Similarity 69.3%;
Matches 278; Conservative (
                                              GI:2170795
                                                        JP 1990222683-A/1. unidentified.
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/codon_start=1
/product-natriuretic peptide"
/product-natriuretic peptide"
/protein_id="abs59258.1"
/db_xref="G1:535705"
/db_xref="G1:535705"
/db_xref="G1:S35705"
/db_xref="G1:S
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Pig (clone pBNP84) natriuretic peptide (BNP) mRNA, complete cds
M233596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 670)

Maekawa, K., Sudoh, T., Furusawa, M., Minamino, N., Kangawa, K., Ohkubo, H., Nakanishi, S. and Matsuo, H.
Cloning and sequence analysis of CDNA encoding a precursor for porcine brain natriuretic peptide
Blochem. Blophys. Res. Commun. 157, 410-416 (1988)
89061744
On Sep 11, 1994 this sequence version replaced di:340970.
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                                                                                          301 ccacgaagccccaagatggtgcaagggtctggctgctttgggaggaagatggaccggatc 360
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                                                                                                                                      1 atggatcoccagacagcaccttcccggggcgctcctgctcctgctcttgcatctggct 60
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Location/Qualifiers
Location/Qualifiers
1. 670
/organism="Sus scrofa"
/db_xref="taxon:9823"
/db_xref="taxon:9823"
/clone="ppNP84"
/tissue_type="atrium"
de 94. 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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Pred. No. 9.1e-36;
0; Mismatches 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       natriuretic peptide.
Sus scrofa atrium cDNA
Sus scrofa
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ilarity 69.3%;
Conservative
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Entrarycts: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Eukarycts: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Entrarycts: Metazoa; Catarrhini; Hominidae; Homo.

Entrarycts: Catarrhini; Hominidae; Homo.

I (bases 1 to 732)

S Mori,T., Maekawa,K., Izumi,A. and Sudo,T.

FRODUCTION OF PHYSIOLOGICALLY ACTIVE PEPTIDE

DAI ICHI PURE CHEM CO LTD, DAI ICHI SEIYAKU CO LTD

OS Homo sapiens (human)

PN JP 1993056794-A.2

PD 09-MAR-1993

PP 09-MAR-1993

CC 12221/02,C12R1:19),C07K99:00;

CC C12221/02,C12R1:19),C07K99:00;

CC C12221/02,Linear;

CC hypothegical: No:.

CC anti-sense: No:.
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                                                 gaggtagccaccgagggcatccgtgggcaccgcaaaatggtcctctacaccctgcgggca
                                                                       325 GAAGCAGCCCCCACGGGGTTCTTGGGCCCCGCAGTAGCATCTTCCAAGTCCTCCGGGGA
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                      265 CGGACGGACCTGGAGCCCCTCCGGCAGGACCGTGGCCTCACAGAAGCCTGGGAGGCGAGG
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                                                                                                                                                                                                                               E04397 732 bp RNA PAT 29-S
DNA sequence encoding human brain natriuretic peptide.
E04397
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                                                                                                                                                  Score 165; DB 5; Le
Pred. No. 7.6e-32;
0; Mismatches 30;
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/db_xref="taxon:9606"
180 c 174 g 174
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Best Local Similarity 85.9%;
Matches 183; Conservative
                                                                                                                                                                                                                                                                                E04397.1 GI:2172598
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PI MORI TOKUO, MAEKAWA KEIJI, IZUMI ATSUSHI, SUDO TETSUJI PC
C12P21/02,C12N15/62//A61K37/02,A61K37/02,A61K37/02,C07K7/10, PC
E04439 732 bp RNA PAT 29-SEP-1997
DNA encoding recombinant hBNP(human Brain Natriuretic Peptide).
E04439
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                                                                                                                                      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 732)
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PRODUCTION OF PHYSIOLOGICALLY ACTIVE PEPTIDE
PATCHT: JP 1993066581-A 2 23-MAR-1993;
DAI ICHI PURE CHEM CO LID, DAI ICHI SEIYAKU CO
S HOMO Sapiens (human)
PN JP 1993068581-A/2
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85.9%; Pred. No. 7.6e-32;
tive 0; Mismatches 30;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
180 c 174 g 17.
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/note='DNA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                  strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
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                                                                  E04439.1 GI:2172640
JP 1993068581-A/2.
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                                                                                                          Homo sapiens.
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PC C12R1:1
CC strande
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CC hypothe
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                   /product="brain natriuretic peptide"
/protein_id="AAA31007.1"
/protein_id="Ti6439"
/db_xxef="cf:16439"
/translation="MGPRMAIPPYLILFIHILIGGRSHPIGGAGIASELPGIGELL
DRINDRYSELQAETIDEPLRODRGITEAWEARBAAPTGVLGPRSSIFQYLRGIRSPK
TWRDSGCFGRRLDRIGSLSGLGCNVLRRY"
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                                                                                     Draft entry and computer-readable sequence [1] kindly submitted by J.J. Seilhamer, 09-FEB-1988.

1. 1479
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     1 (bases 1 to 1479)

Porter, J.G., Arfsten, A.E., Palisi, T., Scarborough, R.M., Lewicki, J.A. and Seilhamer, J.J.

Cloning of a cDNA encoding porcine brain natriuretic peptide 9214071
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Pred. No. 2.5e-25;
0; Mismatches 75; Indels
Eutheria; Cetartiodactyla; Suina; Suidae; Sus
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/gene="BNP"
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/gene="BNP"
94. .162
/gene="BNP"
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                                                                                                                               /organism="Sus scrofa"
/db_xref="taxon:9823"
/tissue_type="atrium"
<1. .218
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719. .1272
/gene="BNP"
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Best Local Similarity 71.0%;
Matches 184; Conservative
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/gene="BNP"
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/gene="BNP"
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640. .717
/gene="BNP"
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Eukaryoffaei mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Vertebrata; Anniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 331)

Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H. Copperative Human Linkage Center
Onpublished (1993)
Synonyms: GCT3H01, CHLC.GCT3H01.T11078
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human STS CHLC.GCT3H01.P11079 clone GCT3H01.

G09534.

G19534.1 GI:941383

STS sequence; primer; sequence tagged site.
human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.
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75 seconds at 55 degrees C
15 seconds at 72 degrees C
27
6 minutes at 72 degress C
                                                                                                                                                                                                                                                                                                                                                               The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@ulowa.edu
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each 1.5 pmole
each 200 uM
0.3 units
10 ul
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/organism="Homo sapiens"
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Primer B: ATCCATGTCTTGGAGGAC
STS size: 124
PCR Profile:
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                                                                                                                                                                                                                                                                                                                            Contact: Dr. Jeffrey C. Murray
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Total Vol:
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PCR cycles:
extension:
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoídea; Bovidae;
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Submitted (OB-DEC-1997) Medicine, University of Otago, Riccarton
Ave, Christchurch, Canterbury, New Zealand
1. .2125
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                  AF037466 2125 bp DNA MAM 24-DEC-1997
Ovis aries brain natriuretic peptide (BNP) gene, complete cds.
AF037466
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                                                                                                                                                                                                                            for Atrial, Brain and
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                                                                                                                                                                                                George, P.M., Espiner, E.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2125;
                                                                                                                                                                                                           cameron, V.A.

The Characterization of Ovine Genes for Atrial, Brain Natriuretic Peptides
Natriuretic Peptides
Onpublished
2 (bases 1 to 2125)
Aitken, G.D., Raizis, A.M., George, P.M., Espiner, E.A.
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Ovis aries"
| Da.xref="taxon:9940"
| Join(<870, .995,1274. .1520,2054. .>2070)
| Gene="BNP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 120.4; DB 3; Length
Pred. No. 1.2e-20;
0; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="brain natriuretic peptide"
<870. .>2070
                                                                                                                                                                Caprinae, Ovis.
1 (bases 1 to 2125)
Aitken, G.D., Raizis, A.M.,
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Best Local Similarity 69.5%;
Matches 182; Conservative (
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                                                                                                                         Ovis aries
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                                                                                                      sheep.
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AF037466
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RESULT DOGBNPA

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (Dases 1 to 1803).
5 Scilhamer, J. J. Arfsten, A. E., Miller, J. A., Lundquist, P., Scarborough, R. M., Lewicki, J. A. and Porter, J. G.
Human and canine gene homologs of porcine brain natriuretic peptide Blochem. Blophys. Res. Commun. 165, 650-658 (1989)
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 DOGBNPA 1803 bp DNA MAM 27-APR-1993 Dog brain natriuretic protein (BNP) gene, complete cds. M31777
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/note-"brain natriuretic protein, intron A"
740. .992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                740. 992

740. 992

7number=2

993. 1554

7note="brain natriuretic protein, intron 1

1555. >1571

7note="brain natriuretic protein"
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1. .1803
/organism="Canis sp."
/db_xref="taxon:9616"
<365. .517
/note="brain natriuretic protein"
join(365. .517,740. .992,1555. .1571)
/codon_start=1
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                                M31777.1 GI:163912
brain natriuretic protein; protein hormone.
Dog DNA, clone D1.
Canis sp.
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DNA encoding human natriuetic peptide.
E05300
E05300.1 GI:2173490
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Best Local Similarity 67.9°
Matches 178; Conservative
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C12P21/06,C07K13/00,C12N1/21,C12N15/16,C12N15/62,C12N15/70, PC
                                                                                                                                                                                                                                              08-MAR-1991 JP 1991043641
YOSHIDA NOBUO, SHIN MASARU, TERAOKA HIROSHI, TAMAKI MIKIO, PI
                                                                                                                                                                                                                                                                                                                                                ASIK37/22, AGIK37/24, (C12N1/21, C12R1:19); Strandedness: Double; topology: Linear; topology: Linear; Feature is identified by similarity; Req. Location/Qualifiers
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                                                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                        1 (bases 1 to 96)
Yoshida,N., Jeraoka,H., Tamaki,M., Inoue,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                _peptide 1..96
/product='natriuetic peptide'.
_location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.9%; Score 96; DB 5; Length 96; Best Local Similarity 100.0%; Pred. No. 2e-14; Matches 96; Conservative 0; Mismatches 0; Indels
                                                                                                                         Watanabe K.
PRODUCTION OF BRAIN NATRIURETIC PEPTIDE PRODUCTION OF BRAIN NATRIURETIC PEPTIDE SHIONOGI & CO LTD
OS Homo saptens (human)
N JP 1993207891-A/1
PD 20-AUG-1993
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/organism="Homo sapiens"
/db_xref="taxon:9606"
23 c 36 g 18
JP 1993207891-A/1.
Homo sapiens.
Homo sapiens
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